

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 12, 2004, 19:27:23 ; Search time 1471.46 Seconds
(without alignments)
10073.859 Million cell updates/sec

Title: US-10-027-725A-1
Perfect score: 342
Sequence: 1 ctcgagctgtgcccaggact.....ccctgggtcacggtctctcca 342

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pln.*
35: em_htg_rod.*
36: em_htg_mam.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	340.4	99.5	342	9	HSA458382	AJ458382 Homo sapi
2	308.4	90.2	342	9	HSA458384	AJ458384 Homo sapi
3	297.2	86.9	342	9	HSA458383	AJ458383 Homo sapi
4	278.2	81.3	432	9	HSA491911	AJ491911 Homo sapi
5	277.2	81.1	411	9	HST22X1	Z75385 H.sapiens m
6	276.6	80.9	432	9	HSA451912	AJ491912 Homo sapi
7	276.4	80.8	351	9	HSA244930	AJ244930 Homo sapi
8	276.4	80.8	360	6	AX061463	AX061463 Sequence
9	275	80.4	414	9	AF062112	AF062112 Homo sapi
10	273.8	80.1	414	9	HST14X13	Z75365 H.sapiens m
11	273.8	80.1	414	9	HST14X4	Z75378 H.sapiens m
12	272	79.5	357	9	HSA244949	AJ244949 Homo sapi
13	271.8	79.5	354	9	HSA245064	AJ245064 Homo sapi
14	271.8	79.5	360	9	HSU80129	U80129 Human immun
15	271.8	79.5	360	9	HSU80130	U80130 Human immun
16	271.6	79.4	358	9	AF021954	AF021954 Homo sapi
17	270.6	79.1	403	12	AF452917	AF452917 Synthetic
18	270.4	79.1	363	9	HSU80131	U80131 Human immun
19	269.2	78.7	354	9	HSA244955	AJ244955 Homo sapi
20	269.2	78.7	417	9	HST14X9	Z75383 H.sapiens m
21	268.8	78.6	366	9	HSA233698	AJ233698 Homo sapi
22	268.6	78.5	351	9	HSA245020	AJ245020 Homo sapi
23	268.4	78.5	357	9	HSA279523	AJ279523 Homo sapi
24	267.4	78.2	400	12	AF452909	AF452909 Synthetic
25	266.8	78.0	357	9	HSA279541	AJ279541 Homo sapi
26	266.2	77.8	412	12	AF452912	AF452912 Synthetic
27	265.8	77.7	366	9	HSA244928	AJ244928 Homo sapi
28	265.8	77.7	369	6	AX061433	AX061433 Sequence
29	265.6	77.7	363	9	HSU80128	U80128 Human immun
30	265.4	77.6	351	9	HSA244958	AJ244958 Homo sapi
31	265.4	77.5	362	9	HSU80169	U80169 Human immun
32	265	77.2	362	9	AF126269	AF126269 Homo sapi
33	264	77.1	351	9	HSA244953	AJ244953 Homo sapi
34	263.8	77.1	406	12	AF453047	AF453047 Synthetic
35	263.6	77.1	357	9	HSA279538	AJ279538 Homo sapi
36	263.4	77.0	362	9	HSU80166	U80166 Human immun
37	263.2	77.0	406	12	AF453217	AF453217 Synthetic
38	262.6	76.8	366	9	HSA279551	AJ279551 Homo sapi
39	262.4	76.7	409	12	AF452947	AF452947 Synthetic
40	262.4	76.6	357	9	HSA244964	AJ244964 Homo sapi
41	262	76.6	360	9	AB063905	AB063905 Homo sapi
42	262	76.6	361	9	HSA279518	AJ279518 Homo sapi
43	261.2	76.4	366	9	HSA244976	AJ244976 Homo sapi
44	261	76.3	366	9	HSU80111	U80111 Human immun
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ALIGNMENTS

RESULT 1
HSA458382
LOCUS HSA458382 342 bp mRNA linear PRI 30-APR-2002
DEFINITION Homo sapiens partial mRNA for immunoglobulin heavy chain variable region (IGHV gene), clone 94.
ACCESSION AJ458382
VERSION AJ458382.1 GI:20387063
KEYWORDS IGHV gene; immunoglobulin heavy chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Flicker,S., Steinberger,P., Norderhaug,L., Sperr,W.R., Majlesi,Y.,
Valent,P., Kraft,D. and Valenta,R.

TITLE Conversion of grass allergen-specific human IgE into a protective
IgG1 antibody
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 342)
AUTHORS Flicker, S.
TITLE Direct Submission
JOURNAL Submitted (24-APR-2002) Flicker S., Department of Pathophysiology,
General Hospital of Vienna, 30, Wahringer Guertel 18-20, A-1090
Vienna, AUSTRIA

FEATURES
source Location/Qualifiers
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/db_xref="GI:20387064"
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/product="immunoglobulin heavy chain variable region"

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Best Local Similarity 99.7%; Pred. No. 1.1e-84;
Matches 341; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTCGAGTCTGGCCAGGACTGGTGAAGCTGCACAGACCCCTCCCTCAGCTGGCGCTGTC 60
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QY 61 TCTGCGGCTCCATCCGAGTGGTGTACTACTCGAGTTGGATCCGCCAACACCCAGGG 120
Db 61 TCTGCGGCTCCATCCGAGTGGTGTACTACTCGAGTTGGATCCGCCAACACCCAGGG 120

QY 121 AAGGCCCTCGAGTGGTGTACTACTCGAGTTGGATCCGCCAACACCCAGGG 180
Db 121 AAGGCCCTCGAGTGGTGTACTACTCGAGTTGGATCCGCCAACACCCAGGG 180

QY 181 CTCAGAGTCGAATTCGCATGTCGAGTGGTGTACTACTCGAGTTGGATCCGCCAACACCCAGGG 240
Db 181 CTCAGAGTCGAATTCGCATGTCGAGTGGTGTACTACTCGAGTTGGATCCGCCAACACCCAGGG 240

QY 241 AACTCTGTGACTGCGCGGACACCGCGGTATTAATCTGTCGAGTTAGATGGCTACACT 300
Db 241 AACTCTGTGACTGCGCGGACACCGCGGTATTAATCTGTCGAGTTAGATGGCTACACT 300

QY 301 TTGGACATCTGGGCGCAGGACCCCTGGTCAACCGTCTCTCA 342
Db 301 TTGGACATCTGGGCGCAGGACCCCTGGTCAACCGTCTCTCA 342

RESULT 2
HSA458384
LOCUS
DEFINITION Homo sapiens partial mRNA for immunoglobulin heavy chain variable
region (IGHV gene), clone 100.
ACCESSION AJ458384
VERSION AJ458384.1 GI:20387067
KEYWORDS IGHV gene; immunoglobulin heavy chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

REFERENCE 1
AUTHORS Flicker, S., Steinberger, P., Norderhaug, L., Sperr, W.R., Majlesi, Y.,
Valent, P., Kraft, D. and Valenta, R.
TITLE Conversion of grass allergen-specific human IgE into a protective
IgG1 antibody
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 342)
AUTHORS Flicker, S.
TITLE Direct Submission
JOURNAL Submitted (24-APR-2002) Flicker S., Department of Pathophysiology,
General Hospital of Vienna, 30, Wahringer Guertel 18-20, A-1090
Vienna, AUSTRIA

FEATURES
source Location/Qualifiers
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/clone="100"
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/db_xref="GI:20387068"
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Best Local Similarity 93.9%; Pred. No. 1e-75;
Matches 321; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 CTCGAGTCTGGCCAGGACTGGTGAAGCTGCACAGACCCCTCCCTCAGCTGGCGCTGTC 60
Db 1 CTCGAGTCTGGCCAGGACTGGTGAAGCTGCACAGACCCCTCCCTCAGCTGGCGCTGTC 60

QY 61 TCTGCGGCTCCATCCGAGTGGTGTACTACTCGAGTTGGATCCGCCAACACCCAGGG 120
Db 61 TCTGCGGCTCCATCCGAGTGGTGTACTACTCGAGTTGGATCCGCCAACACCCAGGG 120

QY 121 AAGGCCCTCGAGTGGTGTACTACTCGAGTTGGATCCGCCAACACCCAGGG 180
Db 121 AAGGCCCTCGAGTGGTGTACTACTCGAGTTGGATCCGCCAACACCCAGGG 180

QY 181 CTCAGAGTCGAATTCGCATGTCGAGTGGTGTACTACTCGAGTTGGATCCGCCAACACCCAGGG 240
Db 181 CTCAGAGTCGAATTCGCATGTCGAGTGGTGTACTACTCGAGTTGGATCCGCCAACACCCAGGG 240

QY 241 AACTCTGTGACTGCGCGGACACCGCGGTATTAATCTGTCGAGTTAGATGGCTACACT 300
Db 241 AACTCTGTGACTGCGCGGACACCGCGGTATTAATCTGTCGAGTTAGATGGCTACACT 300

QY 301 TTGGACATCTGGGCGCAGGACCCCTGGTCAACCGTCTCTCA 342
Db 301 TTGGACATCTGGGCGCAGGACCCCTGGTCAACCGTCTCTCA 342

RESULT 3
HSA458383
LOCUS
DEFINITION Homo sapiens partial mRNA for immunoglobulin heavy chain variable
region (IGHV gene), clone 60.
ACCESSION AJ458383
VERSION AJ458383.1 GI:20387065

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1
Flicker, S., Steinberger, P., Norderhaug, L., Sperr, W.R., Majlesi, Y.,
Valent, P., Kraft, D. and Valenta, R.
TITLE Conversion of grass allergen-specific human IgE into a protective
IgG1 antibody
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 342)
AUTHORS Flicker, S.
TITLE Direct Submission
JOURNAL Submitted (24-APR-2002) Flicker S., Department of Pathophysiology,
General Hospital of Vienna, 30, Wahringer Guertel 18-20, A-1090
Vienna, AUSTRIA

FEATURES
source Location/Qualifiers
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/db_xref="taxon:9606"
/clone="100"
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/product="immunoglobulin heavy chain variable region"

V_region
ORIGIN
Query Match 90.2%; Score 308.4; DB 9; Length 342;
Best Local Similarity 93.9%; Pred. No. 1e-75;
Matches 321; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 CTCGAGTCTGGCCAGGACTGGTGAAGCTGCACAGACCCCTCCCTCAGCTGGCGCTGTC 60
Db 1 CTCGAGTCTGGCCAGGACTGGTGAAGCTGCACAGACCCCTCCCTCAGCTGGCGCTGTC 60

QY 61 TCTGCGGCTCCATCCGAGTGGTGTACTACTCGAGTTGGATCCGCCAACACCCAGGG 120
Db 61 TCTGCGGCTCCATCCGAGTGGTGTACTACTCGAGTTGGATCCGCCAACACCCAGGG 120

QY 121 AAGGCCCTCGAGTGGTGTACTACTCGAGTTGGATCCGCCAACACCCAGGG 180
Db 121 AAGGCCCTCGAGTGGTGTACTACTCGAGTTGGATCCGCCAACACCCAGGG 180

QY 181 CTCAGAGTCGAATTCGCATGTCGAGTGGTGTACTACTCGAGTTGGATCCGCCAACACCCAGGG 240
Db 181 CTCAGAGTCGAATTCGCATGTCGAGTGGTGTACTACTCGAGTTGGATCCGCCAACACCCAGGG 240

QY 241 AACTCTGTGACTGCGCGGACACCGCGGTATTAATCTGTCGAGTTAGATGGCTACACT 300
Db 241 AACTCTGTGACTGCGCGGACACCGCGGTATTAATCTGTCGAGTTAGATGGCTACACT 300

QY 301 TTGGACATCTGGGCGCAGGACCCCTGGTCAACCGTCTCTCA 342
Db 301 TTGGACATCTGGGCGCAGGACCCCTGGTCAACCGTCTCTCA 342

RESULT 3
HSA458383
LOCUS
DEFINITION Homo sapiens partial mRNA for immunoglobulin heavy chain variable
region (IGHV gene), clone 60.
ACCESSION AJ458383
VERSION AJ458383.1 GI:20387065

KEYWORDS	IGHV gene; immunoglobulin heavy chain; variable region.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	1
AUTHORS	Flicker S., Steinberger P., Norderhaug, L., Sperr, W.R., Majlesi, Y., Valent, P., Kraft, D. and Valenta, R.
TITLE	Conversion of grass allergen-specific human IgE into a protective IgG1 antibody
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 342)
AUTHORS	Flicker S.
TITLE	Direct Submission
JOURNAL	Submitted (24-APR-2002) Flicker S., Department of Pathophysiology, General Hospital of Vienna, 3Q, Waehringer Guertel 18-20, A-1090 Vienna, AUSTRIA
FEATURES	Location/Qualifiers
source	1. .342 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="60" /rearranged 1. .342 /gene="IGHV" <1. .>342 /gene="IGHV" /product="immunoglobulin heavy chain" /codon_start=1 /protein_id="CAD30445.1" /db_xref="GI:20387066" /db_xref="REMBL:CAD30445" /translation="LSSGGLVPSQTLSTCTVSGSIRSGGYWVWRQPKGLE WIGNYHSGNTYNNPSLKSRIITMSVDTSKHFSRLTSTAADTAVYYCARSDGYTLDNWQGTLLTVSS"
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CDS	1. .342 /product="immunoglobulin heavy chain variable region"
V_region	1. .342 /gene="IGHV" /product="immunoglobulin heavy chain variable region"
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Best Local Similarity	91.8%; Pred. No. 1.5e-72;
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QY	1 CTCAGTCTGCGCCAGACTGGTGAAGCCCTGCACAGACCCCTGCTCCCTCAGCTGCGTGTG 60
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QY	61 TCTGGCGGCTCCATCCGACGTGGTGTACTACTGGAGTTGGATCCGCCAACACCCAGGG 120
Db	61 TCTGGTGGCTCCATCCGACGTGGTGTATTATTGGAGTTGGGTGGCGCCAGCTCCAGGG 120
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Db	121 AAGGCGCTGGAGTGGATCGGCAACATCTATCACAGTGGGACACCTACTACACCCGTCC 180
QY	181 CTCAGAGTCGAATTGCCATGTGGTAGACACGCTCTGAGAACAGATTCTCCCTGAGCGTG 240
Db	181 CTCAGAGTCGAATTACCATGTGAGTAGACACGCTCTAAGAACCACTTCTCCCTGAGACTG 240
QY	241 AACTCTGTGACTGCGCGGACAGCGCGTGTATTACTGTGCGAGTTAGATGGCTACAT 300
Db	241 ACCTCTGTGACTGCGCGGACAGCGCGTGTATTACTGTGCGGCGTGAATGGGTACT 300
QY	301 TTGACATCTGGGCGCCAGGGAACCTGGTCAACCTGCTCCCTCA 342
Db	301 TTGGACAACTGGGCGCCAGGGAACCTGGTCAACCTGCTCCCTCA 342
RESULT 4	
HSA491911	81.3%; Score 278.2; DB 9; Length 432;
LOCUS	Best Local Similarity 88.8%; Pred. No. 3.2e-67;
DEFINITION	Homo sapiens mRNA for immunoglobulin heavy chain V-D-J-Ce region (clone HD17 C9).
ACCESSION	U491911
VERSION	AU491911.1 GI:24415808
KEYWORDS	constant region; epsilon chain; IGH gene; immunoglobulin heavy chain; variable region.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	1
AUTHORS	Coker, H.A., Durham, S.R. and Gould, H.J.
TITLE	Local somatic hypermutation and class switch recombination in the nasal mucosa of allergic rhinitis patients
JOURNAL	J. Immunol. 171 (10), 5602-5610 (2003)
MEDLINE	22970235
PUBMED	14607969
REFERENCE	2 (bases 1 to 432)
AUTHORS	Coker, H.A.
TITLE	Direct Submission
JOURNAL	Submitted (26-JUN-2002) Coker H.A., Biomedical Sciences, Randall Centre, King's College London, Guy's Campus, London, SE1 1UL, UNITED KINGDOM
FEATURES	Location/Qualifiers
source	1. .432 /organism="Homo sapiens" /mol_type="mRNA" /isolation_source="nasal biopsy from inferior turbinate of allergic rhinitis patient" /db_xref="taxon:9606" /clone="HD17 C9" /sex="female" /cell_type="B lymphocyte" /tissue_type="nasal mucosa" /dev_stage="adult" /rearranged /country="United Kingdom" 1. .432 /gene="IGH" <1. .>432 /gene="IGH" /codon_start=1 /product="immunoglobulin heavy chain V-D-J-Ce region" /protein_id="CAD38020.1" /db_xref="GI:24415809" /db_xref="REMBL:CAD38020" /translation="QVQLQESGFLVKPSQNLSTCTVSGAISSGGYWVWIRQHPG KGLEWIGTYIRGTYNPSLRSLRISIDTSANQFSRLTSLTAADTAVYFCARLDG YSLDYWGQGTLLTVSSASTQSPSVFPLTRCKNIPSNATSVT"
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D_segment	298. .315 /gene="IGHV4-30" /note="DS-24 rf 3"
J_segment	316. .355 /gene="IGHV4-30" /note="region JH4b"
gene	356. .432 /gene="IGHE"
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Query Match	81.3%; Score 278.2; DB 9; Length 432;
Best Local Similarity	88.8%; Pred. No. 3.2e-67;

Matches 301; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 4 GAGTCTGCCCCAGAGCTGGTGAAGCCTGCACAGACCCCTGTCCTCAGCTGGCTGTCTCT 63
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 Db 16 GAGTGGGGCCCCAGGACTGGTGAAGCCTTTCACAGAACCTGTCCCTCAGCTGCTCTCT 75
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 Db 196 AGGAGTGAATTAATCATGTCAATTGACACGCTGCGAATCAGTTCTCCCTGAGGCTGACC 255
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 QY 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGGAGGTTAGATGGCTACACTTTG 303
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 Db 256 TCTGTGACTGCGCGGACACGCGCGTGTATTCTGTGGCGTCTAGATGGGTACAGTTTG 315
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 Db 316 GACTACTGGGCGCAGGGAACCCGTGTACCGTCTCCTCA 354
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RESULT 5
 HST22X1 411 bp mRNA linear PRI 30-APR-1997
 LOCUS H.sapiens mRNA for Ig heavy chain variable region (VH4DJ) (clone T22.1).
 DEFINITION
 ACCESSION Z75385
 VERSION Z75385.1 GI:2062048
 KEYWORDS immunoglobulin; immunoglobulin heavy chain; immunoglobulin superfamily; variable region.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 411)
 AUTHORS Tonnelle,C., D'Arcole,C., Depraetere,V., Metras,D., Boubli,D. and Fougereau,M.
 TITLE Human thymic B cells largely overexpress the VH4 Ig gene family. A possible role in the control of tolerance in situ?
 JOURNAL Int. Immunol. 9 (3), 407-414 (1997)
 MEDLINE 97244170
 PUBMED 9088979
 REFERENCE 2 (bases 1 to 411)
 AUTHORS Tonnelle,C.
 TITLE Direct Submission
 JOURNAL Submitted (26-JUN-1996) Cecile Tonnelle, Centre d'Immunologie Marseille Luminy, Marseille, 13288, France

FEATURES
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 /organism="Homo sapiens"
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 1. .57
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 /note="Ig VH4-segment"
 D_segment 355. .377
 J_segment 378. .411
 ORIGIN

Query Match 81.1%; Score 277.2; DB 9; Length 411;
 Best Local Similarity 88.8%; Pred. No. 6e-67;
 Matches 300; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 4 GAGTCTGCCCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCTCAGCTGGCTGTCTCT 63
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 Db 73 GAGTGGGGCCCCAGGACTGGTGAAGCCTTTCACAGAACCTGTCCCTCAGCTGCTCTCT 132
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 QY 64 GCGGCTCCATCCGCGAGTGGTGGTTACTACTGGAGTTGGATCCGCGCAACACCCAGGGAAG 123
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 Db 133 GGTGGCTCCATCAGCAGTGGTGGTTACTACTGGAGTGGATCCGCGCTCAGCCAGGAAG 192
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 QY 124 GGCCTGGAGTGGATGGGTGATCATCTATCAGAGTGGGAACACTACAAACCCGTCCTC 183
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 Db 193 GGCCTGGAGTGGATGGGTGATCATCTATCAGAGTGGGAACACTACTACAAACCCGTCCTC 252
 |||||
 QY 184 AAGAGTGAATTCGCATGTCGCTAGACACAGCTGTGAGAACAGTTCTCCCTGAGGCTGAAC 243
 |||||
 Db 253 AAGAGTGAATTCGCATGTCGCTAGACACAGCTGTGAGAACAGTTCTCCCTGAGGCTGAAC 312
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 QY 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGGAGGTTAGATGGCTACACTTTG 303
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 Db 313 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGGAGGTTAGTATTGTAGTAGT 372
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 QY 304 GACATCTGGGCGCAGGGAACCCGTGTACCGTCTCCTC 341
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 Db 373 TCCAGCTGGGCGCAGGGAACCCGTGTACCGTCTCCTC 410
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RESULT 6
 HSA491912 432 bp mRNA linear PRI 20-NOV-2003
 LOCUS Homo sapiens mRNA for immunoglobulin heavy chain V-D-J-Ce region (clone HD17 C37).
 DEFINITION
 ACCESSION AJ491912
 VERSION AJ491912.1 GI:24415810
 KEYWORDS constant region; epsilon chain; IGH gene; immunoglobulin heavy chain; variable region.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.
 TITLE Local somatic hypermutation and class switch recombination in the nasal mucosa of allergic rhinitis patients
 JOURNAL J. Immunol. 171 (10), 5602-5610 (2003)
 MEDLINE 22970235
 PUBMED 14607969
 REFERENCE 2 (bases 1 to 432)
 AUTHORS Coker,H.A.
 TITLE Direct Submission
 JOURNAL Submitted (26-JUN-2002) Coker H.A., Biomedical Sciences, Randall Centre, King's College London, Guy's Campus, London, SE1 1UL, UNITED KINGDOM

FEATURES
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /db_xref="taxon:9606"
 /clone="HD17 C37"
 /sex="female"
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 /tissue_type="nasal mucosa"
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Query Match 80.9%; Score 276.6; DB 9; Length 432;
Best Local Similarity 88.5%; Pred. No. 8.9e-67;
Matches 300; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 4 GAGCTGGCCAGGACTGGTGAAGCCCTGCACAGACCCCTGCCCTCAGCTCGCTGTCT 63
Db 16 GAGTCGGGCCAGGACTGGTGAAGCCCTGCACAGACCCCTGCCCTCAGCTGTCT 75
QY 64 GCGGCTCCATCCGAGTGGTGGTTACTACTGAGTTGGATCCGCCAACCCAGGGAAG 123
Db 76 GGTGGGCCCATCAATAGTGGTGGTTACTACTGAGCTGGATCCGCCAACCCAGGGAAG 135
QY 124 GGCTGGAGTGGATGGTGCATCTATCACAGTGGGAACACCTACAAACCCGTCCTC 183
Db 136 GGCTGGAGTGGATGGTGCATCTATCACAGTGGGAACACCTACAAACCCGTCCTC 195
QY 184 AAGAGTCGAATGCCATGTCGGTAGACAGCTCTGAGAACAAAGTTCTCCCTGAGCTGAAC 243
Db 196 AGGAGTCGAATCAATGTCGAATGACAGCTCTGCAATCAGTTCTCCCTGAGCTGAAC 255
QY 244 TCTGTGACTCCGGGACACGGCGGTGTATCTGTGCGAGGTAGATGGCTACACTTG 303
Db 256 TCTGTGACTCCGGGACACGGCGGTGTATCTGTGCGGTCTAGATGGGTACAGTTG 315
QY 304 GACATCTGGGCGCAGGAAACCCCTGGTCACCGTCTCCCTCA 342
Db 316 GACTACTGGGCGCAGGAAACCCCTGGTCACCGTCTCCCTCA 354

RESULT 7
HSA244930 351 bp mRNA linear PRI 01-JUN-2000
LOCUS
DEFINITION Homo sapiens mRNA for immunoglobulin mu heavy chain variable
region, partial, clone 1-A34.
ACCESSION AJ244930
VERSION AJ244930.1 GI:4995319
KEYWORDS IGM; Igm heavy chain; immunoglobulin mu heavy chain; variable
region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1

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```

AUTHORS
Dono, M., Zupo, S., Leanza, N., Melioli, G., Fogli, M., Melagrana, A.,
Chiorazzi, N. and Ferrarini, M.
Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic
marginal zone equivalents
J. Immunol. 164 (11), 5596-5604 (2000)
20281644
PUBMED 10820234
2 (bases 1 to 351)
Dono, M.
Direct Submission
Submitted (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca
sul Cancro, Immunologia Clinica, L.go Rosanna Benzi 10- Genova,
ITALY
FEATURES
Location/Qualifiers
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Best Local Similarity 90.1%; Pred. No. 1e-66;
Matches 308; Conservative 0; Mismatches 31; Indels 3; Gaps 1;

QY 4 GAGTCGGCCAGGACTGGTGAAGCCCTGCACAGACCCCTGCCCTCAGCTCGCTGTCT 63
Db 10 GAGTCGGGCCAGGACTGGTGAAGCCCTGCACAGCCCTGCCCTCAGCTGTCTCT 69
QY 64 GCGGCTCCATCCGAGTGGTGGTTACTACTGAGTTGGATCCGCCAACCCAGGGAAG 123
Db 70 GGTGGCTCCATCAGAGTGGTGGTTACTACTGAGCTGGATCCGCCAACCCAGGGAAG 129
QY 124 GGCTGGAGTGGATGGTGCATCTATCACAGTGGGAACACCTACAAACCCGTCCTC 183
Db 130 GGCTGGAGTGGATGGTGCATCTATCACAGTGGGAACACCTACAAACCCGTCCTC 189
QY 184 AAGAGTCGAATGCCATGTCGGTAGACAGCTCTGAGAACAAAGTTCTCCCTCAGCTGAAC 243
Db 190 AAGAGTCGAATGCCATGTCGGTAGACAGCTCTGAGAACAAAGTTCTCCCTCAGCTGAAC 249
QY 244 TCTGTGACTCCGGGACACGGCGGTGTATCTGTGCGA---GGTTAGATGCTACACT 300
Db 250 TCTGTGACTCCGGGACACGGCGGTGTATCTGTGCGAGAGGAGGAGGACTTCTAC 309
QY 301 TTGGACATCTGGGCGCAGGAAACCCCTGGTCAACCGTCTCTCTCA 342
Db 310 TTGACTACTGGGCGCAGGAAACCCCTGGTCAACCGTCTCTCTCA 351

RESULT 8
AX061463 360 bp DNA linear PAT 22-JAN-2001
LOCUS
DEFINITION Sequence 32 from Patent WO0100678.

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ACCESSION AX061463
VERSION AX061463.1 GI:12406598
KEYWORDS
SOURCE Human immunodeficiency virus 1 (HIV-1)
ORGANISM Human immunodeficiency virus 1
          Human immunodeficiency virus 1
REFERENCE 1
AUTHORS Watkins,B.A. and Reitz,M.S.
TITLE Human monoclonal antibodies to hiv-1 envelope glycoprotein gp120
JOURNAL Patent: WO 0100678-A 32 04-JAN-2001;
          THE GOVERNMENT OF THE UNITED STATES OF AMERICA (US)
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    Matches 308; Conservative 0; Mismatches 31; Indels 3; Gaps 1;
QY 4 GAGTCTGCCAGGACTGGTGAAGCCTGCACAGACCCTGTCCCTCAGCTGGCTGTCTCT 63
Db 19 GAGTCGGGCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGCACCTGTCTCT 78
QY 64 GCGGCTCATCCGACAGTGGTGTACTACTGGAGTTGGATCCGCGCAACACCCAGGGAAG 123
Db 79 GGTGGCTCCATCAGCAGTGGTGTACTACTGGAGTGGATCCGCGCAACACCCAGGGAAG 138
QY 124 GGCCTGGAGTGATGGGTACATCTACAGTGGGAACACCTACAAACCCGTCCTC 183
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QY 184 AAGAGTCGAATGGCCATGTCCGTAGACACGTTGAGAACAAAGTTCTCCCTGAGGCTGAAC 243
Db 199 AAGAGTCGAGTTACCATATCAGTAGACACGTTAAGAACACCAAGTTCTCCCTGAAGCTGAGC 258
QY 244 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGGA---GGTTAGATGGCTACACT 300
Db 259 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGAGAGGGGTAGTAGTGAGCTGG 318
QY 301 TTGACATCTGGGGCCAGGGAACCTGTGTCACCGTCTCCTCA 342
Db 319 TTCGACCCCTGGGCGCAGGGAACCTGTGTCACCGTCTCCTCA 360
RESULT 9
AF062112
LOCUS Homo sapiens clone 21u-26 immunoglobulin heavy chain variable
DEFINITION region (IGH) mRNA, partial cds.
ACCESSION AF062112
VERSION AF062112.1 GI:3170686
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 414)
AUTHORS Wang,X. and Stollar,B.D.
TITLE Immunoglobulin VH gene expression in human aging
JOURNAL Clin. Immunol. 93 (2), 132-142 (1999)
MEDLINE 99459182
PUBMED 10527689
REFERENCE 2 (bases 1 to 414)
AUTHORS Wang,X. and Stollar,B.D.
TITLE Direct Submission
JOURNAL Submitted (22-APR-1998) Biochemistry Department, Tufts University
          School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA
FEATURES
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QY 4 GAGTCTGCCAGGACTGGTGAAGCCTGCACAGACCCTGTCCCTCAGCTGGCTGTCTCT 63
Db 73 GAGTGGGCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGCACCTGTCTCT 132
QY 64 GCGGCTCCATCCGAGTGGTGTACTACTGTGAGTTGGATCCGCAACACCCAGGGAAG 123
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Db 193 GGCCTGGAGTGATGGGTACATCTATTACAGTGGGACACCTACTACAAACCCGTCCTC 252
QY 184 AAGAGTCGAATGGCCATGTCCGTAGACACGTTGAGAACAAAGTTCTCCCTGAGGCTGAAC 243
Db 253 AAGAGTCGAGTTACCATATCAGTAGACACGTTCCAGAACCAAGTTCTCCCTGAGCTGAGC 312
QY 244 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGAGGTAGATGGCTACACTTTG 303
Db 313 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGGTGGGTACACGAGCTGTCTT 372
QY 304 GACATCTGGGCGCAGGGAACCTGTGTCACCGTCTCCTCA 342
Db 373 GACTACTGGGCGCAGGGAACCTGTGTCACCGTCTCCTCA 411
RESULT 10
HST14X13
LOCUS H.sapiens mRNA for Ig heavy chain variable region (VH4DU) (clone
DEFINITION T14.13).
ACCESSION Z75365
VERSION Z75365.1 GI:2062027
KEYWORDS immunoglobulin; immunoglobulin heavy chain; immunoglobulin
          superfamily; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 414)
AUTHORS Tonnellet,C., D'Ercole,C., Depaertere,V., Metras,D., Boublil,L. and
          Fougereau,M.
TITLE Human thymic B cells largely overexpress the VH4 Ig gene family. A

```

possible role in the control of tolerance in situ?

JOURNAL
MEDLINE
PUBMED
REFERENCE
2 (bases 1 to 414)
Tonnelle,C.
Direct Submission
TITLE
JOURNAL
Submitted (26-JUN-1996) Cecile Tonnelle, Centre d'Immunologie
Marseille Luminy, Marseille, 13288, France
FEATURES
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58. .354
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Best Local Similarity 89.7%; Pred. No. 5.4e-66;
Matches 306; Conservative 0; Mismatches 32; Indels 3; Gaps 1;
Qy 4 GAGTCTGCCAGACTGGTGAAGCTGCACAGACCCCTGTCCTCAGTGGCTGTCTCT 63
Db 73 GAGTCGGGCCAGGACTGGTGAAGCTTTCACAGACCCCTGTCCTCAGTGGCTGTCTCT 132
Qy 64 GCGGCTCCATCCGAGTGGTGGTACTACTGGAGTGGATCCGCCAACACCCAGGGAAG 123
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Qy 184 AAGAGTGGATGGATCGGTAGACACGCTCTAGAACCAAGTTCTCCCTGAAGCTGAGC 243
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Qy 244 TCTGTGACTCGCGGACACCGCCGTGTATTACTGTGGAGGTTA---GATGGCTACACT 300
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RESULT 11
HST14X4
LOCUS
DEFINITION H.sapiens mRNA for Ig heavy chain variable region (VH4DJ) (clone T14.4).
ACCESSION Z75378
VERSION 275378.1 GI:2062042
KEYWORDS immunoglobulin; immunoglobulin heavy chain; immunoglobulin superfamily; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 414)
Tonnelle,C., D'Ercole,C., Depraetere,V., Metras,D., Boublil,L. and

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
2 (bases 1 to 414)
Tonnelle,C.
Direct Submission
TITLE
JOURNAL
Submitted (26-JUN-1996) Cecile Tonnelle, Centre d'Immunologie
Marseille Luminy, Marseille, 13288, France
FEATURES
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J_segment
369. .414
ORIGIN

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Best Local Similarity 89.7%; Pred. No. 5.4e-66;
Matches 306; Conservative 0; Mismatches 32; Indels 3; Gaps 1;
Qy 4 GAGTCTGCCAGACTGGTGAAGCTGCACAGACCCCTGTCCTCAGTGGCTGTCTCT 63
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Qy 124 GGCCTGGAGTGGATGGGTACTATCATCAGTGGGAACACTCAACACCCCGTCCCTC 183
Db 193 GGCCTGGAGTGGATGGGTACTATCTATTACGTGGGACACTACTACAAACCCGTCCCTC 252
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Db 253 AAGAGTGGATGGATCGGTAGACACGCTCTAGAACCAAGTTCTCCCTGAAGCTGAGC 312
Qy 244 TCTGTGACTCGCGGACACCGCCGTGTATTACTGTGGAGGTTA---GATGGCTACACT 300
Db 313 TCTGTGACTCGCGGACACCGCCGTGTATTACTGTGGAGGTTAAGGGGTGTCCTCTAC 372
Qy 301 TTGGACATCTGGGCCAGGGAACCCCTGTCACCGTCTCCTC 341
Db 373 TTTGACTCTGGGCCAGGGAACCCCTGTCACCGTCTCCTC 413

RESULT 12
HSA244949
LOCUS
DEFINITION H.sapiens mRNA for immunoglobulin mu heavy chain variable region, partial, clone 3-A5.
ACCESSION AJ244949
VERSION AJ244949.1 GI:4995357
KEYWORDS IGM; IGM heavy chain; immunoglobulin mu heavy chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE
AUTHORS      1
              Dono, M., Zupo, S., Leanza, N., Melioli, G., Fogli, M., Melagrana, A.,
              Chiorazzi, N. and Ferrarini, M.
TITLE        Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic
              marginal zone equivalents
JOURNAL      J. Immunol. 164 (11), 5596-5604 (2000)
MEDLINE      20281644
PUBMED       10820234
REFERENCE    2 (bases 1 to 357)
              Dono, M.
AUTHORS      Direct Submission
TITLE        Submitted (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca
              sul Cancro, Immunologia Clinica, L.go Rosanna Benzi 10- Genova,
              ITALY
FEATURES
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Best Local Similarity 88.8%; Pred. No. 1.7e-65;
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QY      4 GAGTCTGGCCAGGACTGTGAAGCTGCACAGACCTCTCCTCAGCTGCCTGCTCT 63
Db      10 GAGTGGGCCCAGGACTGTGAAGCTTCACAGACCTCTCCTCAGCTGCCTGCTCT 69
QY      64 GCGGCTCCATCCGAGTGGTGTACTACTGGAGTTGGATCCGCCAACACCCAGGGAAG 123
Db      70 GTGTCTCCATCAGCAGTGGTGTACTACTGGAGTTGGATCCGCCAGCACCCAGGGAAG 129
QY      124 GGCCTGGAGTGGTGTACTACTATCAGTGGGACACCTACAAACCCGTCCTC 183
Db      130 GGCCTGGAGTGGTGTACTACTATCAGTGGGACACCTACTACAAACCCGTCCTC 189
QY      184 AAGAGTCGAATTCGCATGTCGTGTAGACAGTCTGAGAACAGTTCTCCCTGAGGCTGAC 243
Db      190 AAGAGTCGAGTTACCATATCAGTAGACAGTCTTAGAACAGTTCTCCCTGAGCTGAGC 249
QY      244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGGAGTTAGAT-----GCG 294
Db      250 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGGAGAGTATATAGAGTATACCAGC 309
QY      295 TACACTTTGACATCTGGGCGCAGGAACCCCTGTCACCGTCTCTCA 342
Db      310 GACTACTTTGACTGTGGGCGCAGGAACCCCTGGTACCGTCTCTCA 357

RESULT 13
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LOCUS       HSA245064      354 bp      mRNA      linear      PRI 02-JUN-1999

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DEFINITION   Homo sapiens mRNA for immunoglobulin gamma heavy chain variable
              region, partial, clone 2-D123.
ACCESSION    AJ245064
VERSION      AJ245064.1 GI:4995589
KEYWORDS     IGG; IGG heavy chain; immunoglobulin gamma heavy chain; variable
              region.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
              Dono, M., Zupo, S., Chiorazzi, N. and Ferrarini, M.
              Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic
              marginal zone equivalents
              Unpublished
              2 (bases 1 to 354)
              Dono, M.
              Direct Submission
              Submitted (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca
              sul Cancro, Immunologia Clinica, L.go Rosanna Benzi 10- Genova,
              ITALY
FEATURES
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QY      4 GAGTCTGCCAGGACTGTGAAGCTGCACAGACCTCTCCTCAGCTGCCTGCTCT 63
Db      16 GAGTCCGCCAGGACTGTGAAGCTTCACAGACCTCTCCTCAGCTGCCTGCTCT 75
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Db      196 AAGAGTCGAGTTACCATATCAGTAGACAGCTCCAAAGAACCACTTCTCCCTGAAACTGAGC 255
QY      244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGGAGTTAGATGGCTTACTTTG 303
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196	Db	196	AAAGAGTCGAGTATACCATATCAGTAGACACGCTCTAAGAACCAAGTTCTCTCCTGAAAGCTGAGC	255
244	QY	244	TCTGTGACTCGCCGGACACGGCGCTGTATTACTGTGGAG-----CTTAGATGGCTAC	297
256	Db	256	TCTGTGACTCGCCGGACACGGCGCTGTATTACTGTGGAGGGGTGAGTGGCTGGTAC	315
298	QY	298	ACTTTGACATCTGGGCGCCAGGAAACCTGGTCAACCGTCTCCTCA	342
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VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
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Homo sapiens				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE				
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JOURNAL				
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Matches				
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89.0%; Pred. No. 2e-65;				
0; Mismatches 32; Indels 6; Gaps 1				
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184	QY	184	AAAGAGTCGAATGCGATGTCGGTAGACACGCTGAGAACAAAGTCTCTCCTGAGGCTGAAC	244
196	Db	196	AAGAGTCGAGTATACCATATCAGTAGACACGCTCTAAGAACACAGTTCTCTCCTCGAAGCTGAGC	255
244	QY	244	TCTGTGACTCGCCGGACACGGCGCTGTATTACTGTGGAG-----CTTAGATGGCTAC	297
256	Db	256	TCTGTGACTCGCCGGACACGGCGCTGTATTACTGTGGAGGGGTGAGTGGCTGGTAC	315
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316	Db	316	TAITTTGACTACTGGGSCCAGGGAACCTGTGTACACCGTCTCCTCA	360
RESULT 15				
HSU80130				
LOCUS				
DEFINITION				
Human immunoglobulin heavy chain variable region (V4-31) gene,				
partial cds.				
ACCESSION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
Homo sapiens (human)				
Homo sapiens				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE				
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GWYFDYWGQGLTVTVSS"				
ORIGIN				
Query Match				
Best Local Similarity				
Matches				
307; Conservative				
79.5%; Score 271.8; DB 9; Length 360;				
89.0%; Pred. No. 2e-65;				
0; Mismatches 32; Indels 6; Gaps 1				
4	QY	4	GAGTCTGGCCAGGACTGGTCAAGCTCGACAGACCTGTCCCTCAGCTGGCTGTCTCT	63
16	Db	16	GAGTCGGGGCCAGGACTGGTGAAGCCTTCACAGACCTGTCCCTCAGCTGTCTCT	75
64	QY	64	GGCGGGTCCATCGCAGCTGTGGTGTACTACTGGAGTGGATCCGCCAACACCCAG	

76	GGTGGCTCCATCAGCAGTGGTGGTTACTCTGGAGCTGGATCCGCAGCACCCAGGGGAG	135
124	GGCCTCGAGTGGATTTGGGTACATCTATCAGTGGGAACACTACAAACCCGTCCTC	183
136	GGCCTCGAGTGGATTTGGGTACATCTATTACAGTGGGAGCACTACTACAAACCCGTCCTC	195
184	AAGAGTTCGAATTCGCATGTCGGTAGACACAGTCTCAGAACCAAGTTCTCCCTCAGGCTGAAC	243
196	AAGAGTCGAGTTACCATATCAGTAGACACAGTCTAAGAACCAGTTCTCCCTCAAGCTGAGC	255
244	TCCTGTCAGTCGCGCGGACAGCGCGTGTATTACTGTGGAG-----GTTAGATGGCTAC	297
256	TCGTGACTCCGCGGACAGCGCCGTGTATTACTGTGGAGGGGTCAGTGGCTGGTAC	315
298	ACTTTGGACATCTGGGCCACGGGAACCCCTGGTCAACCGTCTCCCTCA	342
316	TATTTTGTACTCTGGGCGCAGGGAACCCCTGGTCAACCGTCTCCCTCA	360

Search completed: August 13, 2004, 03:57:58
Job time : 1473.46 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 00:12:28 ; Search time 2005.71 Seconds
(without alignments)
5091.898 Million cell updates/sec

Title: US-10-027-725a-1
Perfect score: 342
Sequence: 1 ctgagctcggccaggact.....ccctggtaaccgctctctca 342

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
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- 13: gb_est4:*
- 14: gb_est5:*
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- 27: em_gss_vri:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	270.2	79.0	832	9	AU122174
2	260.8	76.3	607	12	BM783015
3	256.6	75.0	677	12	BG686767
4	253	74.0	490	14	CD689564

5	250.8	73.3	643	9	AU134293
6	247	72.2	369	10	AW404242
7	246	71.9	509	10	AW406349
8	245.8	71.9	582	10	AW401348
9	244.6	71.5	1108	12	BM920469
10	241.8	70.7	914	12	BG757054
11	240	70.2	363	10	AW403420
12	239.4	70.0	813	13	BQ710364
13	238.2	69.6	903	13	BQ706579
14	237.8	69.5	828	10	BF974568
15	237.2	69.4	890	13	BX324929
16	237.2	69.4	977	13	BX396901
17	237.2	69.4	1201	13	BX336959
18	236.8	69.2	904	13	BQ710488
19	236.2	69.1	814	12	BG685325
20	236.2	69.1	1050	9	AL552672
21	235.2	68.8	447	10	AW402200
22	235.2	68.8	1019	13	BQ072420
23	235	68.7	474	10	AW408410
24	234.8	68.7	596	12	BM817833
25	234.6	68.6	942	13	BQ706244
26	233.8	68.4	661	12	BG686421
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29	233.4	68.2	915	13	BQ706358
30	233.4	68.2	959	13	BH999307
31	233.2	68.2	856	13	BQ421299
32	233	68.1	435	10	BF871158
33	233	68.1	924	12	BG758027
34	232.6	68.0	368	10	AW403989
35	232.2	67.9	357	12	BP432480
36	232.2	67.9	921	13	BQ710000
37	232.2	67.9	925	13	BQ710876
38	231.8	67.8	367	10	AW403544
39	231.8	67.8	924	13	BQ708516
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ALIGNMENTS

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LOCUS	AU122174	MAMMAL	Homo sapiens	cdna clone MAMMAL001802 5', mRNA
DEFINITION	AU122174	sequence.		
ACCESSION	AU122174			
VERSION	AU122174.1	GI:10937409		
KEYWORDS	EST.			
SOURCE	Homo sapiens	(human)		
ORGANISM	Homo sapiens			
REFERENCE	1	(bases 1 to 832)		
AUTHORS	Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T.			
TITLE	HRI human cDNA project			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: Takao Isogai Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 Email: genomics@hri.co.jp HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of			

DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM1618 row: i column: 10
 High quality sequence stop: 675.
 Note: this is a NIH_MGC Library.

FEATURES

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 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
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 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN

Query Match 75.0%; Score 256.6; DB 12; Length 677;
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QY 4 GAGTCGGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCCTCAGCTGCCTGTCTCT 63
 Db 99 GAGTCGGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCCTCAGCTGCCTGTCTCT 158
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 Db 159 GGTGGCTCCATCAGCAGTGGTGTACTACTGGAGTGGATCCGCAACACCCAGGGAAG 217
 QY 124 GCGCTGGAGTGGATGGGTACATCTATCAGTGGGAACACCTACACACCCGTCCTC 183
 Db 218 GGCCTGGAGTGGATGGGTACATCTATCAGTGGGAACACCTACACACCCGTCCTC 277
 QY 184 AAGAGTCGAATTGCCATGTCGGTACACGCTCTGAGAACAGTTCCTCCCTGAGCGTGAAC 243
 Db 278 AAGAGTCGAATTACCATATCAGTAGACGCTCTAAGAACAGTTCCTCCCTGAGCTGAGC 337
 QY 244 TCTGTGACTGCCCGGACACGCGCGGTGTATTACTGTGCGA-----GGTTAGATGGCTAC 297
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 QY 298 ACTTTGGACATCTGGGCGCAGGAAACCCCTGTCACCGTCTCTCTCA 342
 Db 398 GGGTTGACCCCTGGGCGCAGGAAACCCCTGGTCAACCGTCTCTCTCA 442

RESULT 4
 CD689564
 LOCUS 490 bp mRNA linear EST 25-JUN-2003
 DEFINITION EST6087 human nasopharynx Homo sapiens cDNA, mRNA sequence.
 ACCESSION CD689564
 VERSION CD689564.1 GI:32209443
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 490)
 AUTHORS Liu X.-O., Zhou Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and
 Zeng, Y.-X.
 TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
 JOURNAL Unpublished (2003)
 COMMENT Contact: Yixin Zeng
 Cancer Center

Sun Yat-sen University
 651 DongFeng Road East, Guangzhou 510060, China
 Tel: 86-1380-9770-743
 Fax: 86-20-8775-4506
 Email: yxzeng@gzsums.edu.cn.

FEATURES

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 Db 231 GCGTGGAGTGGATGGGTACATCTATCAGTGGGAGTCCGACTACACCCGTCCTCTCA 290
 QY 185 AGAGTCGAATTGCCATGTCGGTAGACAGCTCTGAGAACAAAGTTCTCCCTGAGGCTGAAC 244
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 VERSION AU134293.1 GI:10994832
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 SOURCE Homo sapiens (human)
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 REFERENCE 1 (bases 1 to 643)
 AUTHORS Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
 Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
 Isogai, T.
 TITLE HRI human cDNA project
 JOURNAL Unpublished (2000)
 COMMENT Contact: Takao Isogai
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genomics@hri.co.jp
 HRI human cDNA project; 5' & 3'-end one pass sequencing; Helix
 Research Institute; cDNA library construction; Department of
 Virology, Institute of Medical Science, University of Tokyo, and


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Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

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ORIGIN

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Query Match      71.9%; Score 246; DB 10; Length 509;
Best Local Similarity 84.5%; Pred. No. 5.5e-55;
Matches 289; Conservative 0; Mismatches 50; Indels 3; Gaps 1;

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QY 64 GCGGCTCCATCCGACGTGGTGGTACTACTGGAGTTGGATCCGCCAACACCCAGGGAAG 123
DB 114 GGTGGCTCCATCAGCAGTAGTAGTACTACTGGGGCTGGATCCGCCAGCCCAAGGAAG 173
QY 124 GGCTGGAGTGGATGGGTACATCATCAGAGTGGGAACACCTACACACCCGTCCTC 183
DB 174 GGGCTGGAGTGGATGGGAGTATCTATTATAGTGGGAGCACCTACTACACCCGTCCTC 233
QY 184 AAGAGTCCGATTTGCCATGTCGGTAGACACGCTCTCAGAACAAAGTTCTCCCTGAGGCTGAAC 243
DB 234 AAGAGTCCGATCCCATATCAGTAGACACGCTCCAGAACCAAGTTCTCCCTGAGCTGAGC 293
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DB 294 TCTGTGACCGCGCGGACACGGCGTGTATTACTGTGCGAGACCTCTCTACGAGCCTGG 353
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DB 354 TTGACCCCTGGGCGCAGGAAACCTGTACCGTCTCTCTCA 395

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RESULT 8
LOCUS      AW401348
DEFINITION UI-HF-BKO-aau-d-08-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3055142 5', mRNA sequence.
ACCESSION  AW401348
VERSION     AW401348.1 GI:6920130
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 582)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgabbs@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M.B. Soares Lab
            cDNA Library Arrayed by: M.B. Soares Lab
            DNA Sequencing by: M.B. Soares Lab
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
            Location/Qualifiers
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FEATURES
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/clone_lib="NIH_MGC_36"
/notes="Vector: pW73-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

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ORIGIN

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QY 64 GCGGCTCCAT---CGCAGTGGTGGTACTACTGGAGTTGGATCCGCCAACACCCAGGG 120
DB 94 GGTGGCTCCATCTCAACAGTGGTATTCTCTGGACTTGGATCCGCCAGACCCAGGG 153
QY 121 AAGGCGCTGGAGTGGATTTGGGTACATCTATCACAGTGGGAACACCTACACACCCGTC 180
DB 154 AAGGCGCTGGAGTGGATTTAGCTCTATTACACTGGGAGACCTATTACACCCGTC 213
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DB 214 CTCAAGAGTCCGATTTCCATATCAGTGGACACGCTCTAAGAACCAAGTTCTCCCTGAACCTG 273
QY 241 AACTCTGTGACTCCGCGGACACGGCGTGTATTACTGTGCGAGTTAGATGGCTAC--- 297
DB 274 AGCTCTGTGACTCCGCGGACACGGCCATGATTACTGTGCGAGAGGAGGCTCTACTAT 333
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RESULT 9
LOCUS      BM920469
DEFINITION AGENCOURT 6709612 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5750444
IMAGE:5750444 5', mRNA sequence.
ACCESSION  BM920469
VERSION     BM920469.1 GI:19370848
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1108)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgabbs@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12781 row: g column: 21
            High quality sequence stop: 626.
            Location/Qualifiers
            1..1108

```

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FEATURES
source
1..1108

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5750444"
/lab_host="DH10B"
/clone_lib="NIH_MGC_122"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."

ORIGIN
Query Match 71.5%; Score 244.6; DB 12; Length 1108;
Best Local Similarity 84.1%; Pred. No. 2e-54;
Matches 290; Conservative 0; Mismatches 49; Indels 6; Gaps 1;
QY 4 GAGTCTGCCCGAGGACTGGTGAAGCTGCACAGACCCCTGCTCCCTCAGCTGGCTGTCTCT 63
Db 110 GAGTGGGGCCCGAGGACTGGTGAAGCTTCGGAGACCCCTGCTCCCTCAGCTGTCTCT 169
QY 64 GCGGCTCCATCCGAGTGGTGGTTACTTACTTGGAGTTGGATCCGGCAACACCCAGGGAAG 123
Db 170 GGTGCTCGTCAGCAGTGGTAGTTACTTCTGGAGCTGGATCCGGCAGCCCCCAGGGAAG 229
QY 124 GCGCTGGAGTGGTGGGTACATCTATCAGAGTGGGAACACCTACAAACCCGTCCTC 183
Db 230 GGACTGGAGTGGTGGGTATATCTATTAGAGTGGGAGCACCACCACTACAAACCCCTCCTC 289
QY 184 AAGAGTCGAATTGGCATGTGGTAGACAGCTGTGAGACAGTTCTCCCTGAGGCTGAAC 243
Db 290 AAGAGTCGAGTCACCATATCAGTAGACACGTCACCAAGACCAAGTTCTCCCTGAGCTGAGC 349
QY 244 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGA-----GGTGTAGTGGCTAC 297
Db 350 TCTGTGACCGCTGCGGACACGCGCTGTATTACTGTGCGAGCGGGGGGGGGGGGAGCTAC 409
QY 298 ACTTTGGACATCTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342
Db 410 TACATGGAGCTCTGGGGCAAGGGACCAAGCTGACCGTCACTCTCTCA 454

RESULT 10
BG757054
LOCUS 914 bp mRNA linear EST 15-MAY-2001
DEFINITION 602710478F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4850851 5',
mRNA sequence.
ACCESSION BG757054
VERSION BG757054.1 GI:14067707
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 914)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Plate: LLCMI692 row: 1 column: 20

High quality sequence stop: 854.
Location/Qualifiers
1. .914
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4850851"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.9kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Query Match 70.7%; Score 241.8; DB 12; Length 914;
Best Local Similarity 85.3%; Pred. No. 1e-53;
Matches 296; Conservative 0; Mismatches 42; Indels 9; Gaps 2;
QY 4 GAGTCTGCCCGAGGACTGGTGAAGCTGCACAGACCCCTGCTCCCTCAGCTGGCTGTCTCT 63
Db 93 GAGTGGGGCCCGAGGACTGGTGAAGCTTCACAGACCCCTGCGCCCTCAGCTGTCTCT 152
QY 64 GCGGCTCCATCCGAGTGGTGGTTACTTACTTGGAGTTGGATCCGGCAACACCCAGGGAAG 123
Db 153 GGTGCTCGTCAGCAGTGGTGGTTACTTCTGGAGCTGGATCCGGCAGCCCCA-GGAAG 211
QY 124 GCGCTGGAGTGGTGGGTACATCTATCAGAGTGGGAACACCTACAAACCCGTCCTC 183
Db 212 GCGCTGGAGTGGTGGGAACATCTATACAGTGGGAGCAGCTACTACAACTCCGTCCTC 271
QY 184 AAGAGTCGAATTGGCATGTGGTAGACACGCTGTGAGAACAAAGTTCTCCCTGAGGCTGAAC 243
Db 272 AAGAGTCGAGTTACCATATCAGTAGACACGCTCTAAGAACCAAGTTCTCCCTGAAGCTGAGC 331
QY 244 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGAGGTAGAGTGGCTACACTTTG 303
Db 332 TCTGTGACTGCGCGGACACGCGCTGTATTATTGTGCGAGGGAAGAGCTACCGTGGC 391
QY 304 GACATCT-----GGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342
Db 392 CACGACTTTGACTACTGGGGCCAGGAACCCCTGGTCAACCGTCTCTCTCA 438

RESULT 11
AW403420
LOCUS 363 bp mRNA linear EST 16-FEB-2000
DEFINITION UI-HF-BKO-abe-g-03-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3056068 5', mRNA sequence.
ACCESSION AW403420
VERSION AW403420.1 GI:6922356
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 363)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Plate: LLCMI692 row: 1 column: 20

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/brp/image/image.html
Seq primer: M13 Forward.

FEATURES

Location/Qualifiers

1. .363
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3056068"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC95"
/lab_host="DH10B (LTI)"
/clone_lib="NIH_MGC 36"
/notes="Vector: pT7T3-Pac; Site 1: NotI; Site 2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 70.2%; Score 240; DB 10; Length 363;
Best Local Similarity 90.7%; Pred. No. 1.8e-53;
Matches 255; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTGCACAGACCTGTCCCTCAGCTGGCTGTCTCT 63
DB 34 GAGTCGGGGCCAGGACGGTGAAGCCTTCACAGACCTGTCCCTCAGCTGTCTCT 93
QY 64 GCGCGCTCCATCCGACGTGTGGTTACTACTGGAGTTGGATCGCCAAACCCAGGGAAG 123
DB 94 GTGTGGCTCCATCAGCAGTGTGGTTACTACTGGACCTGGATCGCCAGCAGCGANGAAG 153
QY 124 GGCCTGGAGTGGATTGGGTACATCTATCACAGTGGGAACACCTACAAACCCGTCCTC 183
DB 154 GGCCTGGAGTGGATTGGGTACATCTATCACAGTGGGAGCGCTACTACATCCGTCCTC 213
QY 184 AAGAGTCGAATTGCCATGTCGGTAGACACGTCTGAGAACAAAGTTCTCCCTGAGGCTGAAC 243
DB 214 AAGAGTCGAGTTACCATATCAGTAGACACGTCTAAGAACCAAGTTCTCCCTGAAGCTGAAC 273
QY 244 TCTGTGACTCCGGGACACGGCGGTGTATTACTGTGCGGAG 284
DB 274 TCTGTGACTCCGGGACACGGCGGTGTATTACTGTGTGAG 314

RESULT 12

BQ710364

LOCUS

DEFINITION BQ710364 813 bp mRNA linear EST 16-JUL-2002

5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgabbs-x@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLCM2476 row: m column: 05

High quality sequence stop: 529.

FEATURES

Location/Qualifiers

1. .813
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6282412"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC 113"
/notes="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 70.0%; Score 239.4; DB 13; Length 813;
Best Local Similarity 90.7%; Pred. No. 4.1e-53;
Matches 255; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTGCACAGACCTGTCCCTCAGCTGGCTGTCTCT 63
DB 82 GAGTCGGGGCCAGGACTGGTGAAGCCTTCACAGACCTGTCCCTCAGCTGTCTCT 141
QY 64 GCGCGCTCCATCCGACGTGTGGTTACTACTGGAGTTGGATCGCCAAACCCAGGGAAG 123
DB 142 GTGTGGCTCCATCAGCAGTGTGGTTACTACTGGAGCTGGATCGCCAGCCCGGGAAG 201
QY 124 GGCCTGGAGTGGATTGGGTACATCTATCACAGTGGGAACACCTACAAACCCGTCCTC 183
DB 202 GGCCTGGAGTGGATTGGGTACATCTATCACAGTGGGAGCACCTACTACAAACCCGTCCTC 261
QY 184 AAGAGTCGAATTGCCATGTCGGTAGACACGTCTGAGAACAAAGTTCTCCCTGAGGCTGAAC 243
DB 262 AAGAGTCGAGTTACCATATCAGTAGACACGTCTCAGAACCAAGTTCTCCCTGAAGATGAAC 321
QY 244 TCTGTGACTCCGGGACACGGCGGTGTATTACTGTGCGGAG 284
DB 322 TCTGTGACTCCGGGACACACGGCGGTGTATTCTGTGCGGAG 362

RESULT 13

BQ706579

LOCUS

DEFINITION BQ706579 903 bp mRNA linear EST 16-JUL-2002

5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgabbs-x@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLCM2515 row: p column: 24
High quality sequence start: 4
High quality sequence stop: 584.
Location/Qualifiers

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 12, 2004, 11:40:47 ; Search time 222.818 Seconds
(without alignments)
6520.490 Million cell updates/sec

Title: US-10-027-725A-1

Perfect score: 342
Sequence: 1 ctagctgtgcccaggact.....ccctgtaccgtctctca 342

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq_29Jan04.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002s.*

7: Geneseqn2003as.*

8: Geneseqn2003bs.*

9: Geneseqn2003cs.*

10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	340.4	99.5	342	6	ABK89637 DNA encod
2	308.4	90.2	342	6	ABK89639 DNA encod
3	297.2	86.9	342	6	ABK89638 DNA encod
4	276.4	80.8	360	4	Aaf29076 Human HIV
5	275	80.4	352	9	Adc99786 Anti-huma
6	275	80.4	352	9	Add05390 Anti-MUC1
7	265.8	77.7	369	4	Aaf29046 Human HIV
8	265.4	77.6	352	9	Adc99778 Anti-huma
9	265.4	77.6	352	9	Add05382 Anti-MUC1
10	265.2	77.5	358	9	Adc99798 Anti-huma
11	265.2	77.5	358	9	Add05402 Anti-MUC1
12	260.8	76.3	516	3	Aaa46876 DNA encod
13	256.4	75.0	352	9	Adc99806 Anti-huma
14	256.4	75.0	352	9	Add05410 Anti-MUC1
15	255.6	74.7	357	2	AaQ38670 MAB GAH v
16	254.4	74.4	366	4	Aaf29066 Human HIV
17	250.8	73.3	1644	2	Aaz22434 Human bla
18	250.2	73.2	741	3	Aaz28998 Anti-muri
19	249	72.8	324	4	Abs46332 Human liv
20	249	72.8	631	2	AaQ78969 Human imm
21	248.6	72.7	1567	4	Aac66522 Human imm
22	248.4	72.6	340	6	ABK84446 Human cDN
23	248.4	72.6	340	7	ACA64884 Human Ig

ALIGNMENTS

RESULT 1

ABK89637
ID ABK89637 standard; DNA; 342 BP.

XX ABK89637;

AC ABK89637;

XX 21-OCT-2002 (first entry)

XX DNA encoding human Ige Fab clone 94 heavy chain.

XX Human; fab; ds; gene; antiallergic; vaccine; grass pollen; Phi p 2;

XX timothy grass pollen allergen; passive immunotherapy.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 1..342

XX /tag= a

XX /product= "Fab clone 94 heavy chain"

XX /tag= b

XX /tag= "PR1 region"

XX /tag= c

XX /note= "CDR1 region"

XX /tag= d

XX /note= "PR2 region"

XX /tag= e

XX /note= "PR3 region"

XX /tag= f

XX /note= "CDR2 region"

XX /tag= g

XX /note= "PR3 region"

XX /tag= h

XX /note= "CDR3 region"

XX /tag= i

XX /note= "PR4 region"

XX /tag= j

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XX /note= "PR4 region"

XX /tag= s

XX /note= "PR4 region"

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PD 11-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-SE002908.
XX
PR 29-DEC-2000; 2000SE-00004892.
XX
PA (PHAA ) PHARMACIA DIAGNOSTICS AB.
XX
PI Flicker S, Steinberger P, Kraft D, Valenta R;
XX
DR WPI; 2002-583604/62.
DR P-PSDB; ABG30445.
XX
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX
PS Disclosure; Page 31-32; 45pp; English.
XX
CC This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have anti-allergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergenic patient's IgE
CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The fabs
CC - or a vaccine against a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for blocking the binding of grass pollen allergenic patients
CC IgE antibodies to Phi p 2. The present sequence represents the DNA
CC encoding the human IgG fab, clone 94 heavy chain protein of the invention
XX
SQ Sequence 342 BP; 69 A; 100 C; 98 G; 75 T; 0 U; 0 Other;

Query Match
Best Local Similarity 99.5%; Score 340.4; DB 6; Length 342;
Matches 341; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTCGAGTCTGGCCAGGACTGGTGAAGCTGCACAGACCCCTGCCCTCAGCTGCCTGTC 60
Db 1 CTCGAGTCTGGCCAGGACTGGTGAAGCTGCACAGACCCCTGCCCTCAGCTGCCTGTC 60
QY 61 TCTGGCGCTCCATCCGAGTGGTGTACTACTCGAGTGGATCGGCCAACACCCAGGG 120
Db 61 TCTGGCGCTCCATCCGAGTGGTGTACTACTCGAGTGGATCGGCCAACACCCAGGG 120
QY 121 AAGGCCCTGGAGTGGGTACATCTATCAGTGGGAACACCTACAAACCCGTC 180
Db 121 AAGGCCCTGGAGTGGGTACATCTATCAGTGGGAACACCTACAAACCCGTC 180
QY 181 CTCAGAGTCGAATTCGATGCGTAGACAGCTGAGAACAGTTCTCCCTGAGGCTG 240
Db 181 CTCAGAGTCGAATTCGATGCGTAGACAGCTGAGAACAGTTCTCCCTGAGGCTG 240
QY 241 AACTCTGTGACTGCGCGGACACCGCGTGTATTACTGTGCGAGTTAGTGCTACT 300
Db 241 AACTCTGTGACTGCGCGGACACCGCGTGTATTACTGTGCGAGTTAGTGCTACT 300
QY 301 TTGGACATCTGGGCGCAGGGAACCTGGTTCACCGTCTCTCTCA 342
Db 301 TTGGACATCTGGGCGCAGGGAACCTGGTTCACCGTCTCTCTCA 342

RESULT 2
ABK89639
ID ABK89639 standard; DNA; 342 BP.
XX
AC ABK89639;
XX

```

```

DT 21-OCT-2002 (first entry)
XX
DE DNA encoding human IgE Fab clone 100 heavy chain.
XX
KW Human; fab; ds; gene; anti-allergic; vaccine; grass pollen; Phi p 2;
KW timothy grass pollen allergen; passive immunotherapy.
XX
OS Homo sapiens.
XX
EH Key
FT CDS Location/Qualifiers
FT 1..342 /product= "Fab clone 100 heavy chain"
FT /tag= a
FT misc_feature 7..78 /tag= b
FT /note= "FR1 region"
FT misc_feature 79..99 /tag= c
FT /note= "CDR1 region"
FT misc_feature 100..123 /tag= d
FT /note= "FR2 region"
FT misc_feature 134..141 /tag= e
FT /note= "FR3 region"
FT misc_feature 142..189 /tag= f
FT /note= "CDR2 region"
FT misc_feature 190..285 /tag= g
FT /note= "FR3 region"
FT misc_feature 286..309 /tag= h
FT /note= "CDR3 region"
FT misc_feature 310..342 /tag= i
FT /note= "FR4 region"
XX
WO200253595-A1.
XX
PD 11-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-SE002908.
XX
PR 29-DEC-2000; 2000SE-00004892.
XX
PA (PHAA ) PHARMACIA DIAGNOSTICS AB.
XX
PI Flicker S, Steinberger P, Kraft D, Valenta R;
XX
DR WPI; 2002-583604/62.
DR P-PSDB; ABG30445.
XX
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX
PS Disclosure; Page 33; 45pp; English.
XX
CC This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have anti-allergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergenic patient's IgE
CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The fabs
CC - or a vaccine against a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergic patients

```


RESULT 4
AAF29076
ID AAF29076 standard; DNA; 360 BP.
XX
AC AAF29076;
XX
DT 03-APR-2001 (first entry)
XX
DE Human HIV-1 monoclonal antibody coding sequence SEQ ID NO: 32.
XX
KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
XX envelope glycoprotein; gp120; diagnosis; ds.
XX
OS Homo sapiens.
XX
FN WO200100678-A1.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-US017327.
XX
PR 30-JUN-1999; 99US-0141701P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Watkins BA, Reitz MS;
XX
DR WPI; 2001-112438/12.
DR P-PSDB; AAB62775.
XX
XX Novel human monoclonal antibody immunoreactive with human
PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
PT in biological sample and providing passive immunotherapy to HIV-1
PT infected mammal.
XX
PS Claim 4; Page 45; 81pp; English.
XX
CC The present invention provides the protein and coding sequences for the
CC variable regions of human monoclonal antibodies which are immunoreactive
CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
CC These can be used in diagnosis and therapy of HIV-1 infection
XX
SQ Sequence 360 BP; 73 A; 104 C; 107 G; 76 T; 0 U; 0 Other;
Query Match 80.8%; Score 276.4; DB 4; Length 360;
Best Local Similarity 90.1%; Pred. No. 2e-69; 3; Indels 3; Gaps 1;
Matches 308; Conservative 0; Mismatches 31; Indels 3; Gaps 1;
QY 4 GAGTCTGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCCTCAGCTGGCGTGTCTCT 63
Db 19 GAGTGGGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCCTCAGCTGTCTCT 78
QY 64 GCGGCTCCATCCGAGTGGTGGTTACTACTGGAGTTGGATCCGCAACACCCAGGGAAG 123
Db 79 GGTGGCTCCATCAGCAGTGGTGGTTACTACTGGAGTGGATCCGCAACACCCAGGGAAG 138
QY 124 GGCCTGGAGTGGTGGTACATCTATCAGAGTGGGACACCTACACAAACCCGTCCTC 183
Db 139 GGCCTGGAGTGGTGGTACATCTATCAGAGTGGGACACCTACTACAAACCCGTCCTC 198
QY 184 AAGAGTCGAATGGCATCTCGGTAGACACAGCTCTCGAGAACAAAGTCTCCCTCAGGCTGAAC 243
Db 199 AAGAGTCGAGTTACCATATCAGTAGACAGAGCTTAAGAACACAGTTCTCCCTCAGGCTGAGC 258
QY 244 TCTGTACTGCGCGGACAGCGCGGTGTATTACTGTGCGA---GGTTAGTGGTACTACT 300
Db 259 TCTGTACTGCGCGGACAGCGCGGTGTATTACTGTGCGAGGGGTAGTAGTGACTGG 318
QY 301 TTGACATCTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342
Db 319 TTGACCCCTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 360

RESULT 5
ADC99786
ID ADC99786 standard; DNA; 352 BP.
XX
AC ADC99786;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-human MUC18 antibody heavy chain variable domain DNA SEQ ID 15.
XX
KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
KW lung cancer; human; ds; gene.
XX
OS Homo sapiens.
XX
FN WO2003057838-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041581.
XX
PR 28-DEC-2001; 2001US-0346299P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J;
XX
DR WPI; 2003-587113/55.
DR P-PSDB; ADC99784.
XX
XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease
PT or condition associated with expression of MUC18 in a patient, e.g.
PT tumors, cancers, and other malignancies.
XX
PS Claim 8; SEQ ID NO 15; 78pp; English.
XX
CC The invention relates to a novel isolated monoclonal antibody comprising
CC a heavy or light chain amino acid or a heavy or light chain variable
CC domain where the antibody binds to MUC18. The monoclonal antibody of the
CC invention demonstrates cytostatic activity and may be useful for treating
CC a disease or condition associated with the expression of MUC18 on the
CC cell surface such as tumours, specifically melanoma, oesophageal,
CC pancreatic or colorectal tumours, carcinomas, particularly cervical
CC carcinomas and cervical intraepithelial neoplasia and cancers including
CC colorectal, breast or lung cancer, as well as other malignancies. The
CC current sequence is that of the anti-human MUC18 monoclonal antibody
CC heavy chain variable domain DNA of the invention.
XX
SQ Sequence 352 BP; 73 A; 100 C; 103 G; 76 T; 0 U; 0 Other;
Query Match 80.4%; Score 275; DB 9; Length 352;
Best Local Similarity 90.3%; Pred. No. 5e-69;
Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;
QY 4 GAGTCTGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCCTCAGCTGGCGTGTCTCT 63
Db 16 GAGTGGGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCCTCAGCTGTCTCT 75
QY 64 GCGGCTCCATCCGAGTGGTGGTTACTACTGGAGTTGGATCCGCCAACACCCAGGGAAG 123
Db 76 GGTGGCTCCATCAGCAGTGGTGGTTACTACTGGACTTGGATCCGCCAGCACCAGGGAAG 135
QY 124 GGCCTGGAGTGGATTTGGGTACATCTATCAGTGGGGAACACCTACAAACCCGTCCTC 183
Db 136 GGCCTGGAGTGGATTTGGGTTCATCTATTACAGTGGGAGCACCTACTACAAACCCGTCCTC 195
QY 184 AAGAGTCGAATGGCATGTCCGTAGACACCTCTCAGACAAAGTCTCCCTCAGGCTGAAC 243
Db 196 AAGAGTCGAGTTACCATATCAGTAGACACGCTTAAGAACACGAGTTCTCCCTCAGGCTGAGC 255

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QY 244 TCTGTGACTGCGCGGACACGGCCGCTGTTACTGTGCGAGTTAGATGCTACACTTTG 303
Db 256 TCTGTGACTGCGCGGACACGGCCGCTGTTACTGTGCGAG---AGAGGGAGATGGCTTT 312

QY 304 GACATCTGGGGCCAGGGAACCCCTGGTCACCGTCTCTCTCA 342
Db 313 GACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCTCTCA 351

RESULT 6
ADD05390
ID ADD05390 standard; DNA; 352 BP.
XX
AC ADD05390;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-MUC18 antibody heavy chain variable region DNA, SEQ ID NO 15.
XX
KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain;
KW gene; ds.
XX
OS Homo sapiens.
XX
XX W02003057006-A2.
XX
PD 17-JUL-2003.
XX
XX 26-DEC-2002; 2002WO-US041582.
XX
PR 28-DEC-2001; 2001US-0346460P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J, Bar-Eli M;
XX
XX WPI; 2003-577496/54.
XX
DR P-PSDB; ADD05388.
XX

Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
treating tumors, inhibiting tumor growth, inhibiting cell invasion
associated with melanoma, or increasing survival of an animal having a
metastatic tumor.

XX Disclosure; SEQ ID NO 15; 87pp; English.
XX

The invention relates to a novel monoclonal antibody used for inhibiting
tumour growth in an animal. The tumour inhibition process comprises
selecting an animal in need of treatment for a tumour, providing a
monoclonal antibody comprising a heavy chain amino acid, where the
antibody consists of any one of 10 fully defined sequences of 117-123
amino acids given in the specification, and where the monoclonal antibody
binds MUC18, and contacting the tumour with the antibody resulting in
inhibited proliferation of the cells. The monoclonal antibody has
cytostatic and can be used in the production of a vaccine. The monoclonal
antibodies against the MUC18 antigen are useful for diagnosing and
treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or
tumour metastasis), inhibiting cell invasion associated with melanoma, or
increasing survival of an animal having a metastatic tumour. This
polynucleotide sequence represents the DNA encoding an anti-MUC18
antibody heavy chain, variable region, protein of the invention.

XX Sequence 352 BP; 73 A; 100 C; 103 G; 76 T; 0 U; 0 Other;
SQ

Query Match 80.4%; Score 275; DB 9; Length 352;
Best Local Similarity 90.3%; Pred. No. 5e-69;
Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

QY 4 GAGTCTGCCCGCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCTCAGTGGCTGTCTCT 63
Db 16 GAGTCGGGCCCGCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCTCAGTGGCTGTCTCT 75

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QY 64 GCGGGCTCCATCCGACAGTGGTGGTTACTACTGGAGTTGGATCCGCCAACACCCAGGGAAG 123
Db 76 GGTGGCTCCATCCGACAGTGGTGGTTACTACTGGAGTTGGATCCGCCAACACCCAGGGAAG 135

QY 124 GGCTGGAGTGGATTGGGTACATCTATCACAGTGGGAACACCTACAAACCCCGTCCCTC 183
Db 136 GGCTGGAGTGGATTGGGTTCATCTATTACAGTGGGAGACCTACTACTAACACCCCGTCCCTC 195

QY 184 AAGAGTCGAATTGCCATGTTCGGTAGACACGTCGTAGAACAAAGTTCTCCCTGAGGCTGAAC 243
Db 196 AAGAGTCGAGTTACCATATCAGTAGACACGCTCTAAGAACAGTTCTCCCTGAAGCTGAGC 255

QY 244 TCTGTGACTGCGCGGACACGGCCGCTGTTACTGTGCGAGTTAGATGCTACACTTTG 303
Db 256 TCTGTGACTGCGCGGACACGGCCGCTGTTACTGTGCGAG---AGAGGGAGATGGCTTT 312

QY 304 GACATCTGGGGCCAGGGAACCCCTGGTCACCGTCTCTCTCA 342
Db 313 GACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCTCTCA 351

RESULT 7
AAF29046
ID AAF29046 standard; DNA; 369 BP.
XX
AC AAF29046;
XX
DT 03-APR-2001 (first entry)
XX
DE Human HIV-1 monoclonal antibody coding sequence SEQ ID NO: 2.
XX
KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
KW envelope glycoprotein; gp120; diagnosis; ds.
XX
OS Homo sapiens.
XX
XX W0200100678-A1.
XX
PD 04-JAN-2001.
XX
XX 23-JUN-2000; 2000WO-US017327.
XX
PR 30-JUN-1999; 99US-0141701P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Watkins BA, Reitz MS;
XX
XX WPI; 2001-112438/12.
XX
DR P-PSDB; AAB62745.
XX

Novel human monoclonal antibody immunoreactive with human
immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
in biological sample and providing passive immunotherapy to HIV-1
infected mammal.

XX Claim 4; Page 34-35; 81pp; English.
PS

The present invention provides the protein and coding sequences for the
variable regions of human monoclonal antibodies which are immunoreactive
with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
These can be used in diagnosis and therapy of HIV-1 infection

XX Sequence 369 BP; 75 A; 104 C; 107 G; 83 T; 0 U; 0 Other;
SQ

Query Match 77.7%; Score 265.8; DB 4; Length 369;
Best Local Similarity 87.5%; Pred. No. 2.2e-66;
Matches 307; Conservative 0; Mismatches 32; Indels 12; Gaps 1;

QY 4 GAGTCTGCCCGCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCTCAGTGGCTGTCTCT 63
Db 19 GAGTCGGGCCCGCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCTCAGTGGCTGTCTCT 78

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QY 64 GCGGCTCCATCCGAGTGGTGGTTACTACTGGAGTTGGATCCGCAACACCCAGGGAAG 123
 |||
 Db 79 GGTGGCTCCATCAGCAGTGGTGGTTACTACTGGAGTGGATCCGCAACCCAGGGAAG 138
 |||
 QY 124 GGCCTGGAGTGATGGGTACATCTATACAGTGGGAACACCTACAAACCCGTCCTTC 183
 |||
 Db 139 GGCCTGGAGTGATGGGTACATCTATACAGTGGGAGCACCTACTACAAACCCGTCCTTC 198
 |||
 QY 184 AAGAGTCGAAATGGCCATGTCGGTAGACAGCTCTGAGAACAGTTCTCCCTAGGCTGAAC 243
 |||
 Db 199 AAGAGTCGAGTTTACCATATCAATAGACAGCTTAAGAACAAAGTTCTCCCTGAAGCTGAGC 258
 |||
 QY 244 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGGAGG-----TTAGAT 291
 |||
 Db 259 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGGAGGCGCGGTATTGTGGTGGT 318
 |||
 QY 292 GGCTACATTTGGACATCTGGGGCCAGGGAACCCCTGGTCAACGTCCTCTCA 342
 |||
 Db 319 GATTGCTCCTTTGACTACTTGGGGCCAGGGAACCCCTGGTCACCGTCTCTCTCA 369
 |||

RESULT 8

ADC99778
 ID ADC99778 standard; DNA; 352 BP.

AC ADC99778;

DT 01-JAN-2004 (first entry)

DE Anti-human MUC18 antibody heavy chain variable domain DNA SEQ ID 7.

XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
 KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;
 KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
 KW lung cancer; human; ds; gene.

XX Homo sapiens.

XX WO2003057838-A2.

XX 17-JUL-2003.

PF 26-DEC-2002; 2002WO-US041581.

PR 28-DEC-2001; 2001US-0346299P.

XX (ABGE-) AGENIX INC.

XX Gudas J;

XX WPI; 2003-587113/55.

DR P-PSDB; ADC99776.

XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease
 PT or condition associated with expression of MUC18 in a patient, e.g.
 PT tumors, cancers, and other malignancies.

PS Claim 8; SEQ ID NO 7; 78pp; English.

CC The invention relates to a novel isolated monoclonal antibody comprising
 CC a heavy or light chain amino acid or a heavy or light chain variable
 CC domain where the antibody binds to MUC18. The monoclonal antibody of the
 CC invention demonstrates cytostatic activity and may be useful for treating
 CC a disease or condition associated with the expression of MUC18 on the
 CC cell surface such as tumors, specifically melanoma, oesophageal,
 CC pancreatic or colorectal tumours, carcinomas, particularly cervical
 CC carcinomas and cervical intraepithelial neoplasia and cancers including
 CC colorectal, breast or lung cancer, as well as other malignancies. The
 CC current sequence is that of the anti-human MUC18 monoclonal antibody
 CC heavy chain variable domain DNA of the invention.

XX Sequence 352 BP; 76 A; 102 C; 103 G; 71 T; 0 U; 0 Other;

Query Match 77.6%; Score 265.4; DB 9; Length 352;
 Best Local Similarity 88.5%; Pred No. 2.9e-66;
 Matches 300; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

QY 4 GAGTCTGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCCTCAGCTGCCTGTCTCT 63
 |||
 Db 16 GAGTCTGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCCTCAGCTGCCTGTCTCT 75
 |||
 QY 64 GCGGCTCCATCCGAGTGGTGGTTACTACTGGAGTTGGATCCGCAACACCCAGGGAAG 123
 |||
 Db 76 GGTGGCTCCATCAGCAGTGGTGGTTACTACTGGAGTGGATCCGCAACCCAGGGAAG 135
 |||
 QY 124 GGCCTGGAGTGATGGGTACATCTATACAGTGGGAACACCTACAAACCCGTCCTTC 183
 |||
 Db 136 GGCCTGGAGTGATGGGTACATCTATACAGTGGGAGCACCTACTACAAACCCGTCCTTC 195
 |||
 QY 184 AAGAGTCGAAATGGCCATGTCGGTAGACAGCTCTGAGAACAAAGTTCTCCCTAGGCTGAAC 243
 |||
 Db 196 AAGAGTCGAGTTTACCATATCAATAGACAGCTTAAGAACAAAGTTCTCCCTGAAGCTGAGC 255
 |||
 QY 244 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGGAGTGGATCCGCAACACCCAGGGAAG 303
 |||
 Db 256 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGGAG---AGGGGGAGATGGCTAC 312
 |||
 QY 304 GACATCTGGGCGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342
 |||
 Db 313 AAGTACTGGGCGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 351
 |||

RESULT 9

ADD05382
 ID ADD05382 standard; DNA; 352 BP.

AC ADD05382;

DT 01-JAN-2004 (first entry)

DE Anti-MUC18 antibody heavy chain variable region DNA, SEQ ID No 7.

XX monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
 KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain;
 KW gene; ds.

XX Homo sapiens.

XX WO2003057006-A2.

XX 17-JUL-2003.

PF 26-DEC-2002; 2002WO-US041582.

PR 28-DEC-2001; 2001US-0346460P.

XX (ABGE-) AGENIX INC.

XX Gudas J, Bar-Eli M;

XX WPI; 2003-577496/54.

DR P-PSDB; ADD05380.

XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
 PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
 PT associated with melanoma, or increasing survival of an animal having a
 PT metastatic tumor.

PS Disclosure; SEQ ID NO 7; 87pp; English.

XX The invention relates to a novel monoclonal antibody used for inhibiting
 CC tumour growth in an animal. The tumour inhibition process comprises
 CC selecting an animal in need of treatment for a tumour, providing a
 CC monoclonal antibody comprising a heavy chain amino acid, where the
 CC antibody consists of any one of 10 fully defined sequences of 117-123

XX (ABGE-) ABGENIX INC.
 XX Gudas J, Bar-Eli M;
 XX WPI; 2003-577496/54.
 DR P-PSDB; Add05400.
 XX
 XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
 PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
 PT associated with melanoma, or increasing survival of an animal having a
 PT metastatic tumor.
 XX

PS Disclosure: SEQ ID NO 27; 87pp; English.

XX The invention relates to a novel monoclonal antibody used for inhibiting
 CC tumour growth in an animal. The tumour inhibition process comprises
 CC selecting an animal in need of treatment for a tumour, providing a
 CC monoclonal antibody comprising a heavy chain amino acid, where the
 CC antibody consists of any one of 10 fully defined sequences of 117-123
 CC amino acids given in the specification, and where the monoclonal antibody
 CC binds MUC18, and contacting the tumour with the antibody resulting in
 CC inhibited proliferation of the cells. The monoclonal antibody has
 CC cytostatic and can be used in the production of a vaccine. The monoclonal
 CC antibodies against the MUC18 antigen are useful for diagnosing and
 CC treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or
 CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
 CC increasing survival of an animal having a metastatic tumour. This
 CC polynucleotide sequence represents the DNA encoding an anti-MUC18
 CC antibody heavy chain, variable region, protein of the invention.
 XX

XX Sequence 358 BP; 77 A; 103 C; 101 G; 77 T; 0 U; 0 Other;

Query Match 77.5%; Score 265.2; DB 9; Length 358;
 Best Local Similarity 88.0%; Pred. No. 3.3e-66;
 Matches 301; Conservative 0; Mismatches 38; Indels 3; Gaps 1;
 QY 4 GAGTCTGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCAGCTGGCTGTCTCT 63
 Db 16 GAGTCTGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCAGCTGGCTGTCTCT 75
 QY 54 GCGGCTCCATCCGAGTGGTGTACTACTGGAGTGGATCCGCCAACACCCAGGGAAG 123
 Db 76 GGTGGCTCCATCAACAGTGGTGGTGTACTACTGGAGTGGATCCGCCAACACCCAGGGAAG 135
 QY 124 GGCCTGGAGTGGATGGGTATCATCTATCACAGTGGGAACACTCAACAACCCGTCCTC 183
 Db 136 GGCCTGGAGTGGATGGGTATCATCTATTCAGTGGGAGCACTACTACAACCCGTCCTC 195
 QY 184 AAGAGTCGAATTGCGCATGTGGTAGACACGCTGTGAGAACAAAGTTCTCCCTGAGGCTGAAC 243
 Db 196 AAGAGTCGAATTACCTTATCAGTAGACACGCTTAAGAACCAGTTCTCCCTGAAGCTGAAC 255
 QY 244 TCTGTACTCCGCGGACACGGCGGTGTATTACTGTGGAG---GTTAGATGGGTACTACT 300
 Db 256 TCTATGACTCCGCGGACACGGCGGTGTATTACTGTGGAGATCGGGAAACAGCTGGT 315
 QY 301 TTGACATCTGGGCGCCAGGGAACCCCTGGTCAACCGTCTCCTCA 342
 Db 316 TTGTACTCTGGGCGCCAGGGAACCCCTGGTCAACCGTCTCCTCA 357

RESULT 12
 ID AAA46876
 AC AAA46876 standard; DNA; 516 BP.

XX AAA46876;

XX 03-OCT-2000 (first entry)

XX DNA encoding the heavy chain of immunoglobulin clone 2.1.3.

XX Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;

KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
 KW proliferative disorder; cancer; immunodeficient disorder; ss.

XX Homo sapiens.

XX WO200037504-A2.

XX 29-JUN-2000.

XX 23-DEC-1999; 99WO-US030895.

XX 23-DEC-1998; 98US-0113647P.

XX (PFIZ) PFIZER INC.

XX (ABGE-) ABGENIX INC.

XX Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;

XX Corvalan JR;

XX WPI; 2000-442647/38.

XX P-PSDB; AAY93713.

XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)

XX -4 containing specified heavy and light chain sequences, useful for

XX treating, e.g. immune disorders.

XX Example 2; Fig 1G; 157pp; English.

XX The present sequence encodes a heavy chain of an antibody of the
 CC invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)
 CC -4. Antibodies of the invention are composed of a heavy chain variable
 CC region, comprising a modified contiguous sequence from a FRI-FR3 sequence
 CC encoded by a human VH3-33 family gene. The modifications are contained in
 CC CDR1, CDR2 and/or framework regions. The antibodies may be used to
 CC inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
 CC disorders (e.g. autoimmune disease, diabetes and graft rejection) and
 CC proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
 CC used to up-regulate immune system to up-regulate immunodeficient
 CC disorders

XX Sequence 516 BP; 103 A; 167 C; 142 G; 104 T; 0 U; 0 Other;

Query Match 76.3%; Score 260.8; DB 3; Length 516;
 Best Local Similarity 87.4%; Pred. No. 6.7e-65;
 Matches 299; Conservative 0; Mismatches 37; Indels 6; Gaps 1;

QY 7 TCTGGCCCGAGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCAGCTGGCTGTCTCTGC 66
 Db 1 TCGGGCCCGAGACTGGTGAAGCCTTCACAGATCCTGTCCCTCAGCTGTCTCTGGT 60
 QY 67 GGCTCCCATCCGACGTGGTGGTTACTCTGGAGTTGGATCCGCCAACACCCAGGGAAGGC 126
 Db 61 GGCCTCCATCAGCAGTGGTGGTCACTACTGGAGCTGGATCCGCCAGACCCAGGGAAGGC 120
 QY 127 CTGAGTGGATVGGGTACATCTATCAAGTGGGAACCACTTACAACCCCTCCCTCAAG 186
 Db 121 CTGAGTGGATVGGGTACATCTATTAATTTGGGAACCACTTACTACAACCCCTCCCTCAAG 180
 QY 187 AGTCGAATTCGCATGTCCGTAGACACGCTCTGAGAACCAAGTTCTCCCTGAGGCTGACTCT 246
 Db 181 AGTCGAGTTACCATATCAGTAGACACGCTCTAAGAACCAGTTCTCCCTGAGGCTGACTCT 240
 QY 247 GTGACTCCGCGGACACGGCCGTGTATTACTGTCCGAGGTTAGATGG-----CTACACT 300
 Db 241 GTGACTCCGCGGACACGGCCGTGTATTATTGTCGAGAGATAGTGGGACTACTACCGT 300
 QY 301 TTGACATCTGGGGCCGAGGGAACCCCTGGTCAACCGTCTCCTCA 342
 Db 301 ATAGACGTCTGGGGCCGAGGGAACCCAGGTCAACCGTCTCCTCA 342

RESULT 13
 ADC99806


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ID AC ADC99806 standard; DNA; 352 BP.
XX
AC ADC99806;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-human MUC18 antibody heavy chain variable domain DNA SEQ ID 35.
XX
KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
XX cytotatic; melanoma; oesophageal; pancreatic; colorectal tumour;
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
KW lung cancer; human; ds; gene.
XX
OS Homo sapiens.
XX
PN WO2003057838-A2.
XX
PD 17-JUL-2003.
XX
XX 26-DEC-2002; 2002WO-US041581.
XX
XX 28-DEC-2001; 2001US-0346299P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J;
XX
DR WPI; 2003-587113/55.
DR P-PSDB; ADC99804.
XX
XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease
PT or condition associated with expression of MUC18 in a patient, e.g.
PT tumors, cancers, and other malignancies.
XX
PS Claim 8; SEQ ID NO 35; 78pp; English.
XX
CC The invention relates to a novel isolated monoclonal antibody comprising
CC a heavy or light chain amino acid or a heavy or light chain variable
CC domain where the antibody binds to MUC18. The monoclonal antibody of the
CC invention demonstrates cytostatic activity and may be useful for treating
CC a disease or condition associated with the expression of MUC18 on the
CC cell surface such as tumours, specifically melanoma, oesophageal,
CC pancreatic or colorectal tumours, carcinomas, particularly cervical
CC carcinomas and cervical intraepithelial neoplasia and cancers including
CC colorectal, breast or lung cancer, as well as other malignancies. The
CC current sequence is that of the anti-human MUC18 monoclonal antibody
CC heavy chain variable domain DNA of the invention.
XX
SQ Sequence 352 BP; 77 A; 101 C; 105 G; 69 T; 0 U; 0 Other;

Query Match 75.0%; Score 256.4; DB 9; Length 352;
Best Local Similarity 87.0%; Pred. No. 1.1e-63;
Matches 294; Conservative 0; Mismatches 41; Indels 3; Gaps 1;

QY 5 AGTCTGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCTCAGTGCCTGCTCTCTG 64
DB 17 AGTGGGGCCAGGACTGGTGAAGCCTTCAGAGACCCCTGTCCTCAGTGCCTGCTCTG 76
QY 65 GCGGCTCCATCCGACGAGTGGTGTACTACTGGAGTTGGATCCGCCAACACCCAGGAGG 124
DB 77 GTGGCTCCATCAGCAGTGGTGTACTTACCAGTGGAGTGGATCCGCCAACACCCAGGAGG 136
QY 125 GCCTGGAGTGGTGGTATCATCTATCAGTGGGAACACCTACAAACCCGTCCTCA 184
DB 137 GCCTGGAGTGGTGGTATCATCTATCAGTGGGAACACCTACAAACCCGTCCTCA 196
QY 185 AGACTCGAATTCATGTCGTAGACACGCTGTGAGAACAGTTCTCCTGAGGTGACT 244
DB 197 AGAGTCGAATTACCATATCAGTAGACACGCTGTGAGAACAGTTCTCCTGAGGTGAGCT 256
QY 245 CTGTGACTGCCGGGACACGGCCGTGTATTACTGTGCGAGTTAGATGGCTPACACTTGG 304
DB 257 CTGTGACGGCCGGGACACGGCCGTGTATTACTGTGCGAGTTAGATGGCTPACACTTGG 313

RESULT 14
ADD05410
ID ADD05410 standard; DNA; 352 BP.
XX
AC ADD05410;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-MUC18 antibody heavy chain variable region DNA, SEQ ID No 35.
XX
KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003057006-A2.
XX
PD 17-JUL-2003.
XX
XX 26-DEC-2002; 2002WO-US041582.
XX
XX 28-DEC-2001; 2001US-0346460P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J, Bar-Eli M;
XX
DR WPI; 2003-577496/54.
DR P-PSDB; ADD05408.
XX
XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
XX treating tumors, inhibiting tumor growth, inhibiting cell invasion
XX associated with melanoma, or increasing survival of an animal having a
XX metastatic tumor.
XX
PS Disclosure; SEQ ID NO 35; 87pp; English.
XX
CC The invention relates to a novel monoclonal antibody used for inhibiting
XX tumor growth in an animal. The tumor inhibition process comprises
XX selecting an animal in need of treatment for a tumour, providing a
XX monoclonal antibody comprising a heavy chain amino acid, where the
XX antibody consists of any one of 10 fully defined sequences of 117-123
XX amino acids given in the specification, and where the monoclonal antibody
XX binds MUC18, and contacting the tumour with the antibody resulting in
XX inhibited proliferation of the cells. The monoclonal antibody has
XX cytostatic and can be used in the production of a vaccine. The monoclonal
XX antibodies against the MUC18 antigen are useful for diagnosing and
XX treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or
XX tumour metastasis), inhibiting cell invasion associated with melanoma, or
XX increasing survival of an animal having a metastatic tumour. This
XX polynucleotide sequence represents the DNA encoding an anti-MUC18
XX antibody heavy chain, variable region, protein of the invention.
XX
SQ Sequence 352 BP; 77 A; 101 C; 105 G; 69 T; 0 U; 0 Other;

Query Match 75.0%; Score 256.4; DB 9; Length 352;
Best Local Similarity 87.0%; Pred. No. 1.1e-63;
Matches 294; Conservative 0; Mismatches 41; Indels 3; Gaps 1;

QY 5 AGTCTGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCTCAGTGCCTGCTCTCTG 64
DB 17 AGTGGGGCCAGGACTGGTGAAGCCTTCAGAGACCCCTGTCCTCAGTGCCTGCTCTG 76
QY 65 GCGGCTCCATCCGACGAGTGGTGTACTACTGGAGTTGGATCCGCCAACACCCAGGAGG 124
DB 77 GTGGCTCCATCAGCAGTGGTGTACTTACCAGTGGAGTGGATCCGCCAACACCCAGGAGG 136
```

QY 125 GCTGGAGTGGATTGGGTACATCTATCAGTGGGAACACCTACAAACCCGTCCTCA 184
 |||||
 Db 137 GCTGGAGTGGATTGGGTACATCTATTACGTGGGAGACCTACCAACCCGTCCTCA 196
 |||||
 QY 185 AGAGTCGAATTGCCATGTGGGTAGACAGCTGTGAGAACAAAGTTCTCCCTGAGGCTGAAC 244
 |||||
 Db 197 AGAGTCGAATTACCATATCAGTAGACACGCTTAAGAACCCAGTTCTCCCTGAAGCTGAGCT 256
 |||||
 QY 245 CTGTGACTGCCGCGACACGCGCGTGTATTACTGTGCGAGGTAGATGGCTACACTTTGG 304
 |||||
 Db 257 CTGTGACTGCCGCGACACGCGCGTGTATTACTGTGCGAG--AGGGGAGATGGCTACA 313
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 QY 305 ACATCTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA 342
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 Db 314 GATATGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA 351
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RESULT 15

AAQ38670

ID AAQ38670 standard; cDNA; 357 BP.

XX AAQ38670;

XX 25-MAR-2003 (revised)

DT 06-MAY-1993 (first entry)

XX

DE MAB GAH variable region of heavy chain.

XX Monoclonal antibody; hybridoma; PCR; variable region; constant region;

KW heavy chain; light chain; ss.

XX Synthetic.

XX EP520499-A1.

XX 30-DEC-1992.

PD

XX 26-JUN-1992; 92EP-00110841.

XX 28-JUN-1991; 91JP-00158859.

PR 28-JUN-1991; 91JP-00158860.

PR 28-JUN-1991; 91JP-00158861.

XX

XX (MITU) MITSUBISHI KASEI CORP.

XX

XX Hosokawa S, Tagawa T, Hirakawa Y, Ito N, Nagaike K;

XX

XX WPI; 1993-001328/01.

DR P-PSDB; AAR30143.

XX

XX Human monoclonal antibody specific for a cancer cell membrane surface

PT antigen - prepnd. from a hybridoma obtd. by cell fusion between human

PT lymphocytes derived from cancer patients and mouse myeloma cells.

XX

XX Claim 13; Page 31 + 14-15; 37pp; English.

PS

XX A human MAb specifically binding to a surface antigen of cancer cell

CC membrane comprises variable regions of the heavy and light chains having

CC the amino acid sequences of AAR30143-44 respectively, encoded by DNA

CC sequences AAQ38670 and AAQ33032 respectively. (Updated on 25-MAR-2003 to

CC correct PN field.)

XX

SQ Sequence 357 BP; 73 A; 105 C; 102 G; 77 T; 0 U; 0 Other;

XX

Query Match

Best Local Similarity 74.7%; Score 255.6; DB 2; Length 357;

Matches 295; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

XX

QY 4 GAGTCTGCCGCCGAGGACTGGTGAAGCTGCAGACCCCTGTCCCTCAGCTGGCTGTCTCT 63

|||

Db 16 GAGTCTGCCGCCGAGGACTGGTGAAGCTTCACAGACCCCTGTCCCTCAGCTGTCTCT 75

|||

QY 64 GCGGCTCCATCCGCACTGGTGGTTACTACTGGAGTTGGATCCGCCAACACCCAGGGAAG 123
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 Db 76 GGTGCTCCATCAGCAGTTTGGTTTCTACTGGAATGATCCGCCAGCACCAGGGAAG 135
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 QY 124 GGCCTGGAGTGGATTGGGTACATCTATCAGTGGGAAACACCTACAAACCCGTCCTTC 183
 |||||
 Db 136 GGCCTGGAGTGGATTGGGTACATCTATTACAGTGGGAGCACCTACTACAAACCCGTCCTTC 195
 |||||
 QY 184 AAGATCGAATTGCCATGTCGGTAGACACAGTCTGAGAACAAAGTTCTCCCTGAGGCTGAAC 243
 |||||
 Db 196 AAGATCGAATTACCATATCGCTAGACACAGTCTAAGAGCCAGTTCTCCCTGAAGCTGAGC 255
 |||||
 QY 244 TCTGTGACTGCCGCGACACGCGCGTGTATTACTGTGCGAGTTAGATGGCTACACTTTG 303
 |||||
 Db 256 TCTGTGACTGCCGCGACACGCGCGTGTATTACTGTGCGAGTTAGATGGCTACACTTTG 303
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 QY 304 ---GACATCTGGGGCCAGGGAACCCCTGTCTACCGTCTCCTCA 342
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 Db 316 GCTGACTACTGGGGCCAGGGAACCAATGGTCAACCGTCTCTTCA 357
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Job time : 226.818 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 03:58:10 ; Search time 760.173 Seconds
(without alignments)
2207.472 Million cell updates/sec

Title: US-10-027-725A-1

Perfect score: 342

Sequence: 1 ctgagctcgccaggact.....ccctggcaccgtctctca 342

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3225727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters: 6451454

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
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- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	342	100.0	342	15	US-10-027-725A-1
2	310	90.6	342	15	US-10-027-725A-3
3	298.8	87.4	342	15	US-10-027-725A-2
4	275	80.4	352	15	US-10-330-613-15
5	275	80.4	352	15	US-10-330-530-15
6	275	80.4	352	17	US-10-660-357-15
7	265.4	77.6	352	15	US-10-330-613-7
8	265.4	77.6	352	15	US-10-330-530-7
9	265.4	77.6	352	17	US-10-660-357-7
10	265.2	77.5	358	15	US-10-330-613-27
11	265.2	77.5	358	15	US-10-330-530-27
12	265.2	77.5	358	17	US-10-660-357-27
13	264.6	77.4	663	10	US-09-972-656-79
14	264.4	77.3	370	16	US-10-309-762-189
					Sequence 189, Appl

15	262.2	76.7	361	16	US-10-309-762-191	Sequence 191, App
16	261.4	76.4	429	16	US-10-309-762-110	Sequence 110, App
17	259.6	75.9	370	16	US-10-309-762-186	Sequence 186, App
18	259.4	75.8	367	16	US-10-309-762-195	Sequence 195, App
19	256.4	75.0	352	15	US-10-330-613-35	Sequence 35, Appl
20	256.4	75.0	352	15	US-10-330-530-35	Sequence 35, Appl
21	256.4	75.0	352	17	US-10-660-357-35	Sequence 35, Appl
22	256.4	75.0	370	16	US-10-309-762-200	Sequence 200, App
23	255.2	74.6	376	16	US-10-309-762-187	Sequence 187, App
24	254.8	74.5	370	16	US-10-309-762-201	Sequence 201, App
25	254.8	74.5	370	16	US-10-309-762-212	Sequence 212, App
26	253.8	74.2	370	16	US-10-309-762-185	Sequence 185, App
27	253.6	74.2	376	16	US-10-309-762-184	Sequence 184, App
28	253.6	74.2	376	16	US-10-309-762-197	Sequence 197, App
29	253.6	74.2	376	16	US-10-309-762-199	Sequence 199, App
30	250.6	73.3	382	16	US-10-309-762-194	Sequence 194, App
31	249.4	72.9	352	16	US-10-309-762-203	Sequence 203, App
32	249.4	72.8	324	9	US-09-864-761-31244	Sequence 31244, A
33	248.4	72.6	519	16	US-10-309-762-174	Sequence 174, App
34	247.8	72.5	450	15	US-10-390-986-13	Sequence 13, Appl
35	245.8	71.9	381	17	US-10-312-316-64	Sequence 64, Appl
36	245.8	71.9	384	17	US-10-312-316-68	Sequence 68, Appl
37	244.2	71.4	381	17	US-10-312-316-66	Sequence 66, Appl
38	243	71.1	361	16	US-10-309-762-193	Sequence 193, App
39	241	70.5	1543	9	US-09-800-729-74	Sequence 74, Appl
40	240.4	70.3	333	9	US-09-925-299-198	Sequence 198, App
41	240.4	70.3	333	10	US-09-925-299-198	Sequence 198, App
42	239.2	69.9	378	9	US-09-974-449-5	Sequence 5, Appl
43	233.6	68.3	462	17	US-10-693-629-47	Sequence 47, Appl
44	230.6	67.4	349	12	US-10-269-711-2	Sequence 2, Appl
45	229.8	67.2	356	17	US-10-388-214A-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1

US-10-027-725A-1
; Sequence 1, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-027-725A-1

Query Match 100.0%; Score 342; DB 15; Length 342;
Best Local Similarity 100.0%; Pred. No. 6.6e-101;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CTCGAGTCTGGCCAGGACTGGTGAAGCTTGACAGACCTGTCCTCAGCTCGCTGTC	60
Db	1	CTCGAGTCTGGCCAGGACTGGTGAAGCTTGACAGACCTGTCCTCAGCTCGCTGTC	60
QY	61	TCCTGGGGGTCCATCCGACAGTGGTGTACTACTGTGAGTTGGATCCGCAACACCCAGGG	120
Db	61	TCCTGGGGGTCCATCCGACAGTGGTGTACTACTGTGAGTTGGATCCGCAACACCCAGGG	120
QY	121	AAGGGCTGGAGTGGATTGGGTACATCTATCAGTGGGAACACCTACAAACCCGTCC	180
Db	121	AAGGGCTGGAGTGGATTGGGTACATCTATCAGTGGGAACACCTACAAACCCGTCC	180
QY	181	CTCAAGATCGAATGCCATGTCGGTAGACACGTCTGTGAGAACAGTTCTCCCTGAGGCTG	240

Db 181 CTCAGAGTCGAATTCGATCGGTAGACACGCTGAGAACAGTTCTCCCTGAGGCTG 240
Qy 241 AACTCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGTTAGATGGCTACT 300
Db 241 AACTCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGTTAGATGGCTACT 300
Qy 301 TTGGACATCTGGGCGCGGAAACCTGCTACCGTCTCTCTCA 342
Db 301 TTGGACATCTGGGCGCGGAAACCTGCTACCGTCTCTCTCA 342

RESULT 2

US-10-027-725A-3
; Sequence 3, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-027-725A-3

Query Match 90.6%; Score 310; DB 15; Length 342;
Best Local Similarity 94.2%; Pred. No. 1.7e-90;
Matches 322; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 1 CTCGAGTCTGGCCAGGACTGGTGAAGCTGCACAGACCCCTGCTCCCTCAGCTGCGCTGTC 60
Db 1 CTCGAGTCTGGCCAGGACTGGTGAAGCTTCACAGACCCCTGCTCCCTCAGCTGCTGTC 60
Qy 61 TCTGCGGCTCATCCGAGTGGTGTACTTACTGTGAGTTGATCGGCAACACCCAGG 120
Db 61 TCTGCGGCTCATCCGAGTGGTGTATTACTTGGAGTTGATCGGCGAGCTCCAGG 120
Qy 121 AAGGSCCTGGAGTGGTGTACATCATCAGTGGGAACACCTACAAACCCGTC 180
Db 121 AAGGSCCTGGAGTGGTGTACATCATCAGTGGGAACACCTACAAACCCGTC 180
Qy 181 CTCAGAGTCGAATTCGATGCGGTAGACACGCTGAGAACAGTTCTCCCTGAGGCTG 240
Db 181 CTCAGAGTCGAATTCGATGCGGTAGACACGCTGAGAACAGTTCTCCCTGAGGCTG 240
Qy 241 AACTCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGTTAGATGGCTACT 300
Db 241 AACTCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGTTAGATGGCTACT 300
Qy 301 TTGGACATCTGGGCGCGGAAACCTGCTACCGTCTCTCTCA 342
Db 301 TTGGACATCTGGGCGCGGAAACCTGCTACCGTCTCTCTCA 342

RESULT 3

US-10-027-725A-2
; Sequence 2, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29

; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-027-725A-2

Query Match 87.4%; Score 298.8; DB 15; Length 342;
Best Local Similarity 92.1%; Pred. No. 7.2e-87;
Matches 315; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 1 CTCGAGTCTGGCCAGGACTGGTGAAGCTGCACAGACCCCTGCTCCCTCAGCTGCGCTGTC 60
Db 1 CTCGAGTCTGGCCAGGACTGGTGAAGCTTCACAGACCCCTGCTCCCTCAGCTGCTGTC 60
Qy 61 TCTGCGGCTCATCCGAGTGGTGTACTTACTGTGAGTTGATCGGCAACACCCAGG 120
Db 61 TCTGCGGCTCATCCGAGTGGTGTATTATTGGAGTTGAGTTCGCGAGCTCCAGG 120
Qy 121 AAGGSCCTGGAGTGGTGTACATCATCAGTGGGAACACCTACAAACCCGTC 180
Db 121 AAGGSCCTGGAGTGGTGTACATCATCAGTGGGAACACCTACAAACCCGTC 180
Qy 181 CTCAGAGTCGAATTCGATGCGGTAGACACGCTGAGAACAGTTCTCCCTGAGGCTG 240
Db 181 CTCAGAGTCGAATTCGATGCGGTAGACACGCTGAGAACAGTTCTCCCTGAGGCTG 240
Qy 241 AACTCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGTTAGATGGCTACT 300
Db 241 AACTCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGTTAGATGGCTACT 300
Qy 301 TTGGACATCTGGGCGCGGAAACCTGCTACCGTCTCTCTCA 342
Db 301 TTGGACATCTGGGCGCGGAAACCTGCTACCGTCTCTCTCA 342

RESULT 4

US-10-330-613-15
; Sequence 15, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-613-15

Query Match 80.4%; Score 275; DB 15; Length 352;
Best Local Similarity 90.3%; Pred. No. 3.9e-79;
Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

Qy 4 GAGTCTGGCCAGGACTGGTGAAGCTGCACAGACCCCTGCTCCCTCAGCTGCGCTGCTCT 63
Db 16 GAGTCTGGCCAGGACTGGTGAAGCTTCACAGACCCCTGCTCCCTCAGCTGCTCTCT 75
Qy 64 GCGGCTCATCCGAGTGGTGTACTTACTGTGAGTTGATCGGCAACACCCAGGAG 123
Db 76 GGTGCTCATCAGCAGTGGTGGTGTACTTACTGTGAGTTGATCGGCAACACCCAGGAG 135
Qy 124 GGCCTGGAGTGGGTATCATCTATCAGTGGGAACACCTACAAACCCGCTCCCTC 183
Db 136 GGCCTGGAGTGGGTATCATCTATCAGTGGGAACACCTACTACAAACCCGCTCCCTC 195

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QY 184 AAGAGTCGAATTGCCATTCGCTAGACACGCTGAGAACAAAGTTCTCCTGAGGCTGAAC 243
Db 196 AAGAGTCGAGTTACCATATCAGTACACACGCTAGAACACGTTCTCCTGAGGCTGAGC 255
QY 244 TCTGTGACTGCGCGGACACGCGCGGTGATTACTGTGGAGTTAGATGGCTACACTTTG 303
Db 256 TCTGTGACTGCGCGGACACGCGCGGTGATTACTGTGGAGTTAGATGGCTGAGTTT 312
QY 304 GACATCTCGGCGCAGGGAACCTGCTACCGTCTCTCA 342
Db 313 GACTACTGGGCGCAGGGAACCTGCTACCGTCTCTCA 351

RESULT 5
US-10-330-530-15
; Sequence 15, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-10-330-530-15
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Query Match 80.4%; Score 275; DB 15; Length 352;
Best Local Similarity 90.3%; Pred. No. 3.9e-79;
Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

QY 4 GAGTCTGCCCGCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCTCAGTGGCTGTCTCT 63
Db 16 GAGTCTGCCCGCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCTCAGTGGCTGTCTCT 75
QY 64 GCGGCTCCATCCGACGTGGTGGTACTACTGAGTTGGATCCGCCAACACCCAGGGAAG 123
Db 76 GGTGGCTCCATCAGCAGTGGTGGTACTACTGAGTTGGATCCGCCAACACCCAGGGAAG 135
QY 124 GCGCTGAGTGGATTGGGTACATCTATCAGTGGGACACCTACACAAACCCGTCCTC 183
Db 136 GCGCTGAGTGGATTGGGTTCATCTATTACGTGGGAGCACCTACTACAAACCCGTCCTC 195
QY 184 AAGAGTCGAATTGCCATTCGCTAGACACGCTCTGAGAACAAAGTTCTCCTGAGGCTGAAC 243
Db 196 AAGAGTCGAGTTACCATATCAGTACACACGCTTAAGAACAGTTCTCCTGAGGCTGAGC 255
QY 244 TCTGTGACTGCGCGGACACGCGCGGTGATTACTGTGGAGTTAGATGGCTACACTTTG 303
Db 256 TCTGTGACTGCGCGGACACGCGCGGTGATTACTGTGGAGTTAGATGGCTGAGTTT 312
QY 304 GACATCTCGGCGCAGGGAACCTGCTACCGTCTCTCA 342
Db 313 GACTACTGGGCGCAGGGAACCTGCTACCGTCTCTCA 351
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RESULT 6
US-10-660-357-15
; Sequence 15, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
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; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-10-660-357-15
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Query Match 80.4%; Score 275; DB 17; Length 352;
Best Local Similarity 90.3%; Pred. No. 3.9e-79;
Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

QY 4 GAGTCTGCCCGCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCTCAGTGGCTGTCTCT 63
Db 16 GAGTCTGCCCGCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCTCAGTGGCTGTCTCT 75
QY 64 GCGGCTCCATCCGACGTGGTGGTACTACTGAGTTGGATCCGCCAACACCCAGGGAAG 123
Db 76 GGTGGCTCCATCAGCAGTGGTGGTACTACTGAGTTGGATCCGCCAACACCCAGGGAAG 135
QY 124 GCGCTGAGTGGATTGGGTACATCTATCAGTGGGACACCTACACAAACCCGTCCTC 183
Db 136 GCGCTGAGTGGATTGGGTTCATCTATTACGTGGGAGCACCTACTACAAACCCGTCCTC 195
QY 184 AAGAGTCGAATTGCCATTCGCTAGACACGCTCTGAGAACAAAGTTCTCCTGAGGCTGAAC 243
Db 196 AAGAGTCGAGTTACCATATCAGTACACACGCTTAAGAACAGTTCTCCTGAGGCTGAGC 255
QY 244 TCTGTGACTGCGCGGACACGCGCGGTGATTACTGTGGAGTTAGATGGCTACACTTTG 303
Db 256 TCTGTGACTGCGCGGACACGCGCGGTGATTACTGTGGAGTTAGATGGCTGAGTTT 312
QY 304 GACATCTCGGCGCAGGGAACCTGCTACCGTCTCTCA 342
Db 313 GACTACTGGGCGCAGGGAACCTGCTACCGTCTCTCA 351
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RESULT 7
US-10-330-613-7
; Sequence 7, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-10-330-613-7
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Query Match 77.6%; Score 265.4; DB 15; Length 352;
Best Local Similarity 88.5%; Pred. No. 5.2e-76;
Matches 300; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

QY 4 GAGTCTGCCCGCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCTCAGTGGCTGTCTCT 63
Db 16 GAGTCTGCCCGCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCTCAGTGGCTGTCTCT 75
QY 64 GCGGCTCCATCCGACGTGGTGGTACTACTGAGTTGGATCCGCCAACACCCAGGGAAG 123
Db 76 GGTGGCTCCATCAGCAGTGGTGGTACTTACCACTGGAGTGGATCCGCCAACACCCAGGGAAG 135
QY 124 GCGCTGAGTGGATTGGGTACATCTATCAGTGGGACACCTACTACAAACCCGTCCTC 183
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Db 136 GGCCTGAGTGGATGGTACATCTATTACAGTGGGACCTACTACAACCGCTCCCTC 195
Qy 184 AAGAGTCGAATGGCATGTGGTAGACACGCTGTGAGAAAGTTCCTCAGGTGAAC 243
Db 196 AAGAGTCGAGTTACCATATCAGTAGACACGCTAAGAACCACTGCTCCCTGAAGCTGAGC 255
Qy 244 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGAGTTAGATGGCTACACTTTG 303
Db 256 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGAG---AGGGGAGATGGCTAC 312
Qy 304 GACATCTGGGCGCAGGGAACCTGTGTACCGTCTCCTCA 342
Db 313 AAGTACTGGGCGCAGGGAACCTGTGTACCGTCTCCTCA 351

RESULT 8
US-10-330-530-7
; Sequence 7, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; FILE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-530-7

Query Match 77.6%; Score 265.4; DB 15; Length 352;
Best Local Similarity 88.5%; Pred. No. 5.2e-76;
Matches 300; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

Qy 4 GAGTCTGGCCAGGACTGTGAAGCTGCACAGACCCCTGTCCCTCAGCTGGCTGTCTCT 63
Db 16 GAGTCGGGCCAGGACTGTGAAGCTTCACAGACCCCTGTCCCTCAGCTGTCTCT 75
Qy 64 GCGGCTCCATCCGAGTGGTGTACTACTGGAGTTCGATCCGCAACACCCAGGGAAG 123
Db 76 GGTGGCTCCATCAGCAGTGGTACTTACCACTGGAGCTGGATCCGCGACACCCAGGGAAG 135
Qy 124 GGCCTGGAGTGGATGGGTACATCTATCACAGTGGGAACACCTACAACACCCGTCCTC 183
Db 136 GGCCTGGAGTGGATGGGTACATCTATCACAGTGGGAACACCTACAACACCCGTCCTC 195
Qy 184 AAGAGTCGAATGGCATGTGGTAGACACGCTGTGAGAAAGTTCCTCAGGTGAAC 243
Db 196 AAGAGTCGAGTTACCATATCAGTAGACACGCTAAGAACCACTGCTCCCTGAAGCTGAGC 255
Qy 244 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGAGTTAGATGGCTACACTTTG 303
Db 256 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGAG---AGGGGAGATGGCTAC 312
Qy 304 GACATCTGGGCGCAGGGAACCTGTGTACCGTCTCCTCA 342
Db 313 AAGTACTGGGCGCAGGGAACCTGTGTACCGTCTCCTCA 351
```

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RESULT 9
US-10-660-357-7
; Sequence 7, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; FILE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
```

```
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-660-357-7

Query Match 77.6%; Score 265.4; DB 17; Length 352;
Best Local Similarity 88.5%; Pred. No. 5.2e-76;
Matches 300; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

Qy 4 GAGTCTGGCCAGGACTGTGAAGCTGCACAGACCCCTGTCCCTCAGCTGGCTGTCTCT 63
Db 16 GAGTCGGGCCAGGACTGTGAAGCTTCACAGACCCCTGTCCCTCAGCTGTCTCT 75
Qy 64 GCGGCTCCATCCGAGTGGTGTACTACTGGAGTTCGATCCGCAACACCCAGGGAAG 123
Db 76 GGTGGCTCCATCAGCAGTGGTACTTACCACTGGAGCTGGATCCGCGACACCCAGGGAAG 135
Qy 124 GGCCTGGAGTGGATGGGTACATCTATCACAGTGGGAACACCTACAACACCCGTCCTC 183
Db 136 GGCCTGGAGTGGATGGGTACATCTATCACAGTGGGAACACCTACAACACCCGTCCTC 195
Qy 184 AAGAGTCGAATGGCATGTGGTAGACACGCTGTGAGAAAGTTCCTCAGGTGAAC 243
Db 196 AAGAGTCGAGTTACCATATCAGTAGACACGCTAAGAACCACTGCTCCCTGAAGCTGAGC 255
Qy 244 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGAGTTAGATGGCTACACTTTG 303
Db 256 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGAG---AGGGGAGATGGCTAC 312
Qy 304 GACATCTGGGCGCAGGGAACCTGTGTACCGTCTCCTCA 342
Db 313 AAGTACTGGGCGCAGGGAACCTGTGTACCGTCTCCTCA 351

RESULT 10
US-10-330-613-27
; Sequence 27, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; FILE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-613-27

Query Match 77.5%; Score 265.2; DB 15; Length 358;
Best Local Similarity 88.0%; Pred. No. 6e-76;
Matches 301; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

Qy 4 GAGTCTGGCCAGGACTGTGAAGCTGCACAGACCCCTGTCCCTCAGCTGGCTGTCTCT 63
Db 16 GAGTCGGGCCAGGACTGTGAAGCTTCACAGACCCCTGTCCCTCAGCTGTCTCT 75
Qy 64 GCGGCTCCATCCGAGTGGTGTACTACTGGAGTTCGATCCGCAACACCCAGGGAAG 123
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Db 76 GGTGGCTCCATCAACAGTGGTGGTGTCTACTGGAGCTGGATCCGCCACGACCCAGGGAAG 135
Qy 124 GGCTGGAGTGGATTGGGTACTATCATCAGTGGGAACACTACAACACCCGTCCTC 183
Db 136 GGCTGGAGTGGATTGGGTACTATCATCAGTGGGAACACTACAACACCCGTCCTC 195
Qy 184 AAGAGTGAATTGGCATTCGGGTAGACACGCTCTGAGAACAAAGTTCTCCCTGAGGCTGAAC 243
Db 196 AAGAGTGAATTACCTTATCAGTAGACACGCTCTAGAACCAAGTTCTCCCTGAAGCTGAAC 255
Qy 244 TCTGTAGTCCGGGACACGGCCGTGTATTACTGTGCGAG---GTTAGATGGCTACACT 300
Db 256 TCTATGACTCGCGGACACGGCCGTGTATTACTGTGCGAGAGATCGGGAACAGCTGGT 315
Qy 301 TTGGACATCTGGGCCAGGGAACCTGGTCAACCGTCTCCTCA 342
Db 316 TTTGACTACTGGGCCAGGGAACCTGGTCAACCGTCTCCTCA 357

RESULT 11
US-10-530-27
; Sequence 27, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX 031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; PRIOR FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-530-27

Query Match 77.5%; Score 265.2; DB 15; Length 358;
Best Local Similarity 88.0%; Pred. No. 6e-76;
Matches 301; Conservative 0; Mismatches 38; Indels 3; Gaps 1;
Qy 4 GAGTCTGGCCAGGACTGGTGAAGCCCTGCAGACACCTGTCCCTCAGCTGGGTGTCTCT 63
Db 16 GAGTGGGCCAGGACTGGTGAAGCCCTGCAGACACCTGTCCCTCAGCTGGGTGTCTCT 75
Qy 64 GGCGGCTCCATCCGACGTGGTGTACTACTGGAGTTGGATCCGCCAACCCAGGGAAG 123
Db 76 GGTGGCTCCATCAACAGTGGTGGTGTCTACTGGAGCTGGATCCGCCAGACCCAGGGAAG 135
Qy 124 GGCTGGAGTGGATTGGGTACTATCATCAGTGGGAACACTACAACACCCGTCCTC 183
Db 136 GGCTGGAGTGGATTGGGTACTATCATCAGTGGGAGCACCTACTACAACCCGTCCTC 195
Qy 184 AAGAGTGAATTGGCATTCGGGTAGACACGCTCTGAGAACAAAGTTCTCCCTGAGGCTGAAC 243
Db 196 AAGAGTGAATTACCTTATCAGTAGACACGCTCTAGAACCAAGTTCTCCCTGAAGCTGAAC 255
Qy 244 TCTGTAGTCCGGGACACGGCCGTGTATTACTGTGCGAG---GTTAGATGGCTACACT 300
Db 256 TCTATGACTCGCGGACACGGCCGTGTATTACTGTGCGAGAGATCGGGAACAGCTGGT 315
Qy 301 TTGGACATCTGGGCCAGGGAACCTGGTCAACCGTCTCCTCA 342
Db 316 TTTGACTACTGGGCCAGGGAACCTGGTCAACCGTCTCCTCA 357

RESULT 12
US-10-660-357-27
; Sequence 27, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:

; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-660-357-27

Query Match 77.5%; Score 265.2; DB 17; Length 358;
Best Local Similarity 88.0%; Pred. No. 6e-76;
Matches 301; Conservative 0; Mismatches 38; Indels 3; Gaps 1;
Qy 4 GAGTCTGGCCAGGACTGGTGAAGCCCTGCAGACACCTGTCCCTCAGCTGGGTGTCTCT 63
Db 16 GAGTGGGCCAGGACTGGTGAAGCCCTGCAGACACCTGTCCCTCAGCTGGGTGTCTCT 75
Qy 64 GGCGGCTCCATCCGACGTGGTGTACTACTGGAGTTGGATCCGCCAACCCAGGGAAG 123
Db 76 GGTGGCTCCATCAACAGTGGTGGTGTCTACTGGAGCTGGATCCGCCAGACCCAGGGAAG 135
Qy 124 GGCTGGAGTGGATTGGGTACTATCATCAGTGGGAGCACCTACTACAACCCGTCCTC 183
Db 136 GGCTGGAGTGGATTGGGTACTATCATCAGTGGGAGCACCTACTACAACCCGTCCTC 195
Qy 184 AAGAGTGAATTGGCATTCGGGTAGACACGCTCTGAGAACAAAGTTCTCCCTGAGGCTGAAC 243
Db 196 AAGAGTGAATTACCTTATCAGTAGACACGCTCTAGAACCAAGTTCTCCCTGAAGCTGAAC 255
Qy 244 TCTGTAGTCCGGGACACGGCCGTGTATTACTGTGCGAG---GTTAGATGGCTACACT 300
Db 256 TCTATGACTCGCGGACACGGCCGTGTATTACTGTGCGAGAGATCGGGAACAGCTGGT 315
Qy 301 TTGGACATCTGGGCCAGGGAACCTGGTCAACCGTCTCCTCA 342
Db 316 TTTGACTACTGGGCCAGGGAACCTGGTCAACCGTCTCCTCA 357

RESULT 13
US-09-972-656-79
; Sequence 79, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Teal, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 79
; LENGTH: 663
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(663)
US-09-972-656-79

Query Match 77.4%; Score 264.6; DB 10; Length 663;
Best Local Similarity 86.9%; Pred. No. 1.1e-75;
Matches 291; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY	4	GAGTCTGGCCGAGGACTGGTGAAGCCTGCA	CAGACCCCTGTCCCTCAGCTGGCGTGTCTCT	63
Db	16	GAGTCTGGCCGAGGACTGGTGAAGCCTT	TCGGAGACCCCTGTCCCTCAGCTGGCGTGTCTCT	75
QY	64	GGCGGCTCCATCCGACAGTGGTGGTTACT	TACTGGAGTTGGATCCGGCAACACCCAGGGAAG	123
Db	76	GGTGGCTCCATCAGCAGTGGTGGTTACTCT	TGGAGCTGGATCCGGCAGCACCAAGGAAG	135
QY	124	GGCCTGAGAGTGGATTGGGTACATCTAT	CACAGTGGGAACAAGTACAAACCCGTCCCTC	183
Db	136	GGCCTGAGTGGATTGGGTACATCTATCAT	TATGGGAGCACTACTACAACCCGTCCCTC	195
QY	184	AAGAGTCCAAATGGCAATCTCGGTAGACA	CAGTCTGAGAACCAAGTTCTCCCTGAGGCTGAAC	243
Db	196	AAGAGTCCAGTCCACCAATCAGTAGACA	GGTCCCAAGAACCAAGTTCTCCCTGAAGCTGAGC	255
QY	244	TCTGTGACTGCCGGGACACGGCCGTGTATT	ACTGTGCGAGGTAGATGGCTACACTTTG	303
Db	256	TCTGTGACCGCGGGGACACGGCCGTGTATT	ACTGTGCGAGGGGACTGGGGCTACTTTT	315
QY	304	GACATCTGGGCCACGGGAACCTGGTCCAC	CGCTCTC	338
Db	316	GACTACTGGGCCACGGGAACCTGGTCCAC	CGCTCTC	350

```

RESULT 14
US-10-309-762-189
; Sequence 189, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 245
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 189
; LENGTH: 370
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-309-762-189

```

```

QY      289  GATGGCTACACTTGGACATCTGGGGCCAGGGACCCCTGGTCACCGTCTCTCTCA 342
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      316  GAAAGACTACGGTGTGGACGTCTGGGGCCAAAGGGACCAACGGTCAACCGTCTCTCTCA 369

RESULT 15
US-10-309-762-191
; Sequence 191, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;   APPLICANT: Gudas, Jean
;   APPLICANT: Foltz, Ian
;   APPLICANT: Handa, Masahisa
;   APPLICANT: Gallo, Michael
;   TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
;   TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
;   FILE REFERENCE: AGENIX.027A
;   CURRENT APPLICATION NUMBER: US/10/309,762
;   CURRENT FILING DATE: 2002-12-02
;   PRIOR APPLICATION NUMBER: 60/337275
;   PRIOR FILING DATE: 2001-12-03
;   NUMBER OF SEQ ID NOS: 246
;   SOFTWARE: Fast-SEQ for Windows Version 4.0
;   SEQ ID NO 191
;   LENGTH: 361
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-309-762-191

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Search completed: August 13, 2004, 19:18:20
Job time : 761.173 secs

QY 301 TTGGACATCTGGGGCCAGGGAACCTGGTACCGCTCTCTCA 342
Db 301 ATAGACGCTGGGGCCAGGGAACCGGTACCGCTCTCTCA 342

RESULT 2
US-08-360-125-3
; Sequence 3, Application US/08360125
; Patent No. 5767246
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Yoshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5767246hiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,125
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human
; CELL TYPE: antibody GAH
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:

CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-3
Query Match 74.7%; Score 255.6; DB 1; Length 357;
Best Local Similarity 86.3%; Pred. No. 2e-70; 44; Indels 3; Gaps 1;
Matches 295; Conservative 0; Mismatches 44; Indels 3; Gaps 1;
QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCCTCAGCTGCCTCTCTCT 63
Db 16 GAGTGGGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCCTCAGCTGCCTCTCTCT 75
QY 64 GCGGCTCCATCCGAGTGGTGGTGTACTAGTGGATTCGGCCACACCCAGGGAAG 123
Db 76 GGTGGCTCCATCAGCAGTGGTGGTGTACTAGTGGATTCGGCCACACCCAGGGAAG 135
QY 124 GGCCTGGAGTGGATTCAGTATCTATCAGTGGAGAACCTACAAACCCGTCCTC 183
Db 136 GGCCTGGAGTGGATTCAGTATCTATCAGTGGAGAACCTACAAACCCGTCCTC 195
QY 184 AAGAGTCGAATTGCCATGTGGTAGACACGTCTGAGAACAGTTCTCCCTGAGGTGAAC 243
Db 196 AAGAGTCGAATTGCCATGTGGTAGACACGTCTGAGAACAGTTCTCCCTGAGGTGAAC 255
QY 244 TCTGTGACTGCGCGGACACGCGCGGTATTAATCTGTGGAGGTAGTAGGTACACTTTG 303
Db 256 TCTGTGACTGCGCGGACACGCGCGGTATTAATCTGTGGAGGTAGTAGGTACACTTTG 315
QY 304 ---GACATCTGGGCGGAGGAAACCTGGTCAACCGTCTCTCA 342
Db 316 GCTGACTACTGGGCGGAGGAAATGGTCAACCGTCTCTCA 357
RESULT 3
US-08-450-578-3
; Sequence 3, Application US/08450578
; Patent No. 5837845
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Yoshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5837845hiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:

Db 256 TCTCTGACTGCGGGACACGGCGGTGTATTACTGTGGAGGTCTACCCGACTACGGGG 315
Qy 304 ---GACATCTGGGCGGAGGAAACCTGTGTACCGTCTCTCA 342
Db 316 GCTGACTACTGGGCGGAGGAAACATGTGTACCGTCTCTCA 357

RESULT 5
US-09-014-880-3
; Sequence 3, Application US/09014880
; Patent No. 5990297
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA et al.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
; TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., #800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/014,880
; FILING DATE: January 28, 1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/450,578
; FILING DATE: May 25, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELEPHONE: 202-721-8200
; TELEFAX: 202-721-8250
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; CELL TYPE: Hybridoma producing human
; CELL TYPE: antibody GAH
US-09-014-880-3

Query Match 74.7%; Score 255.6; DB 2; Length 357;
Best Local Similarity 86.3%; Pred. No. 2e-70;
Matches 295; Conservative 0; Mismatches 44; Indels 3; Gaps 1;
Qy 4 GAGTCTGGCCAGGACTGTGAGGCTGCACAGACCTGTCCCTCAGCTGCGTGTCT 63
Db 16 GAGTGGGCCAGGACTGTGAGGCTGCACAGACCTGTCCCTCAGCTGCGTGTCT 75
Qy 64 GCGGCTCCATCCGCGAGTGTGTACTGTGATCGCCACACCCAGGGAAG 123
Db 76 GGTGGCTCCATCAGAGTGTGTGTTTCTACTGGAGTGGATCGCCAGGGAAG 135

Qy 124 GGCTTGAGTGGATTGGTACATCTATCAGTGGGAAACCTACAAACCCGCTCCTC 183
Db 136 GGCTTGAGTGGATTGGTACATCTATTTACAGTGGGAGCACTACTACAAACCCGCTCCTC 195
Qy 184 AAGAGTCGAATTGCGCATGTGCGGTAGACACAGTCTGAGAAACAAGTTCTCCCTGAGGCTGAAC 243
Db 196 AAGAGTCGAGTTACCATATCGTATAGACACAGTCTAAGAGCCAGTTCTCCCTGAAGCTGAGC 255
Qy 244 TCTGTGACTGCGGCGGACACGGCGGTGTATTACTGTGGAGGTGTAGATGGCTACACTTTG 303
Db 256 TCTGTGACTGCGGCGGACACGGCGGTGTATTACTGTGGAGGTGTACCCGACTACGGGG 315
Qy 304 ---GACATCTGGGCGGAGGAAACCTGTGTACCGTCTCTCTCA 342
Db 316 GCTGACTACTGGGCGGAGGAAACATGTGTACCGTCTCTCTCA 357

RESULT 6
US-08-450-363-3
; Sequence 3, Application US/08450363
; Patent No. 6436434
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Yoshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 6436434ihiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,363
; FILING DATE: May 25, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:

ORGANISM: ;
STRAIN: ;
INDIVIDUAL ISOLATE: ;
DEVELOPMENTAL STAGE: ;
HAPLOTYPE: ;
TISSUE TYPE: ;
CELL TYPE: Hybridoma producing human ;
CELL TYPE: antibody GAH ;
CELL LINE: ;
ORGANELLE: ;
IMMEDIATE SOURCE: ;
LIBRARY: ;
CLONE: ;
POSITION IN GENOME: ;
CHROMOSOME/SEGMENT: ;
MAP POSITION: ;
UNITS: ;
FEATURE: ;
NAME/KEY: ;
LOCATION: ;
IDENTIFICATION METHOD: ;
OTHER INFORMATION: ;
PUBLICATION INFORMATION: ;
AUTHORS: ;
TITLE: ;
JOURNAL: ;
VOLUME: ;
ISSUE: ;
PAGES: ;
DATE: ;
DOCUMENT NUMBER: ;
FILING DATE: ;
PUBLICATION DATE: ;
RELEVANT RESIDUES IN SEQ ID NO: ;
US-08-450-363-3

Query Match 74.7%; Score 255.6; DB 4; Length 357;
Best Local Similarity 86.3%; Pred. No. 2e-70;
Matches 295; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCAGAGCTGGTGAAGCTGCACAGACCCCTGTCCTCAGCTGGCTGTCTCT 63
DB 16 GAGTCGGGCCAGAGCTGGTGAAGCTGCACAGACCCCTGTCCTCAGCTGGCTGTCTCT 75

QY 64 GGCGGCTCCATCCCGAGTGGTGTACTACTGGAGTTGGATCCGCCACACCCAGGGAAG 123
DB 76 GGTGGCTCCATCAGCAGTTGGTGTCTACTGGAACTGGATCCGCCAGACCCAGGGAAG 135

QY 124 GGCTGGAGTGGATTGGGTATCATCTATCAGTGGGAACTACAAACCCCTGCTC 183
DB 136 GGCTGGAGTGGATTGGGTATCATCTATCAGTGGGAGCCTACTACTACACCCCTGCTC 195

QY 184 AAGAGTCGAATTGCCATGTGGTGTAGACACGCTCTGAGAACAAAGTTCTCCCTGAGGCTGAAC 243
DB 196 AAGAGTCGAGTTACCATATCGCTAGACACGCTCTAAGAGCAGTTCTCCCTGAGCTGAGC 255

QY 244 TCTGTACTGCGCGGACAGCGCGTGTATCTACTGTGGAGTTAGTGGTACACTTG 303
DB 256 TCTGTACTGCGCGGACAGCGCGTGTATCTACTGTGGAGTTAGTGGTACACTTG 315

QY 304 ---GACATCTGGGCGCAGGGAACCCCTGTCACCCCTCTCTCA 342
DB 316 GCTGACTACTGGGCGCAGGGAACATGTCACCCGTCTCTCA 357

RESULT 7
US-08-545-809A-31
; Sequence 31, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE

TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 631 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: human lymphoblast
CELL LINE: CGM1
US-08-545-809A-31

Query Match 72.8%; Score 249; DB 3; Length 631;
Best Local Similarity 92.9%; Pred. No. 3e-68;
Matches 261; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 4 GAGTCTGGCCAGAGCTGGTGAAGCTGCACAGACCCCTGTCCTCAGCTGGCTGTCTCT 63
DB 305 GAGTCGGGCCAGAGCTGGTGAAGCTGCACAGACCCCTGTCCTCAGCTGGCTGTCTCT 364

QY 64 GGCGGCTCCATCCCGAGTGGTGTACTACTGGAGTTGGATCCGCCACACCCAGGGAAG 123
DB 365 GGTGGCTCCATCAGCAGTTGGTGTACTACTGGAGCTGGATCCGCCAGACCCAGGGAAG 424

QY 124 GGCTGGAGTGGATTGGGTATCATCTATCAGTGGGAACTACAAACCCCTGCTC 183
DB 425 GGCTGGAGTGGATTGGGTATCATCTATCAGTGGGAGCCTACTACTACAAACCCCTGCTC 484

QY 184 AAGAGTCGAATTGCCATGTGGTGTAGACACCTCTGAGAACAAAGTTCTCCCTGAGGCTGAAC 243
DB 485 AAGAGTCGAGTTACCATATCAGTAGACACCTCTAAGNACCAGTTCTCCCTGAGGCTGAGC 544

QY 244 TCTGTACTGCGCGGACAGCGCGTGTATCTACTGTGGAG 284
DB 545 TCTGTACTGCGCGGACAGCGCGTGTATCTACTGTGGAG 585

RESULT 8
US-09-049-672A-17
; Sequence 17, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti

APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-Seq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1567 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PANTUT01
CLONE: 1513264
US-09-049-672A-17

Query Match 72.7%; Score 248.6; DB 3; Length 1567;
Best Local Similarity 84.0%; Pred. No. 5.7e-68;
Matches 300; Conservative 0; Mismatches 39; Indels 18; Gaps 1;
QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCTCAGCTGGCGTGTCTCT 63
Db 150 GAGTGGGCCAGGACTGGTGAAGCCTTCGGAGACCTGTCCTCAGCTGGCGTGTCTCT 209
QY 64 GCGGCTCCATCCGAGTGGTGTACTACTGGAGTTGGATCGGCAACACCCAGGGAAG 123
Db 210 GGTGGCTCCATCACTAGTGGTGTACTACTGGAGCTGGATCGGCAACCCAGGGAAG 269
QY 124 GGCCTGGAGTGGATGGGTACATCTATCAGTGGGAACACCTACAGAACCCGTCCTC 183
Db 270 GGCCTGGAGTGGATGGGTACATCTATCAGTGGGAACCCCTACAGAACCCGTCCTC 329
QY 184 AGAGTCGAATTCGCCATGTCGGTAGACAGTCTGAGAACAAAGTTCCTCCCTGAGGCTGAAC 243
Db 330 AGAGTCGAGTTACCATATACAGTAGACAGTCCAGAACAGTTCTCCCTGAGGCTGAGC 389
QY 244 TCTGTGACTGCGCGGACACCGCCGTGTATTACTGTGCGAGGTAGATG----- 292
Db 390 TCTGTGACTGCGCGGACACCGCCGTGTATTACTGTGCGAGAGATGAGTGTAAAG 449
QY 293 -----GTACACTTTGGACATCTGGGCGCAGGGAACCTGTGTCACCGTCTCCTCA 342
Db 450 GGGGGGAACCTACCGTATGGACGCTGGGGCCAGGGAACCTGTGTCACCGTCTCCTCA 506

RESULT 9

US-09-582-337-13
; Sequence 13, Application US/09582337
; Patent No. 6562618
; GENERAL INFORMATION:
; APPLICANT: Japan Tobacco, Inc.
; TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
; TITLE OF INVENTION: and Medicinal Uses Thereof
; FILE REFERENCE: J1-009PCT
; CURRENT APPLICATION NUMBER: US/09/582,337
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: JP P1997-367699
; PRIOR FILING DATE: 1997-12-25
; PRIOR APPLICATION NUMBER: JP P1998-356183
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(450)
; NAME/KEY: sig_peptide
; LOCATION: (1)..(58)
; NAME/KEY: V_region
; LOCATION: (59)..(353)
US-09-582-337-13

Query Match 72.5%; Score 247.8; DB 4; Length 450;
Best Local Similarity 85.7%; Pred. No. 6.1e-68;
Matches 306; Conservative 32; Mismatches 32; Indels 19; Gaps 2;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCTCAGCTGGCGTGTCTCT 63
Db 74 GAGTGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGT-CCTCACCTGCACTGTCTCT 132
QY 64 GCGGCTCCATCCGAGTGGTGTACTACTGGAGTTGGATCGGCAACACCCAGGGAAG 123
Db 133 GGTGGCTCCATCAGCAGTGGTGTACTACTGGAGCTGGATCGGCAACCCAGGGAAG 192
QY 124 GGCCTGGAGTGGATGGGTACATCTATCAGTGGGAACACCTACAAACCCGTCCTC 183
Db 193 GGCCTGGAGTGGATGGGTACATCTATCAGTGGGAACACCTACTACAAACCCGTCCTC 252
QY 184 AGAGTCGAATTCGCATGTCGGTAGACAGTCTGAGAACAAAGTTCCTCCCTGAGGCTGAAC 243
Db 253 AAGAGTCGAGTTACCATATCAGTAGACAGCTTAAGAACCCAGTTCTCCCTGAAGCTGAGC 312
QY 244 TCTGTGACTGCGCGGACACCGCCGTGTATTACTGTGCGAGGT----- 286
Db 313 TCTGTGACTGCGCGGACACCGCCGTGTATTACTGTGCGAGGTATTACTATGATAGTGT 372
QY 287 -TAGATGGCTACATTTTGGACATCTGGGCGCAGGGAACCCCTGGTCAACCGTCTCCTCA 342
Db 373 GGTATTACGACTACTTTGACTACTGGGCGCAGGGAACCCCTGGTCAACCGTCTCCTCA 429

RESULT 10

US-09-800-729-74
; Sequence 74, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: PZ044PI
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22

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; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
; LENGTH: 1543
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-800-729-74

Query Match          70.5%; Score 241; DB 4; Length 1543;
Best Local Similarity 82.2%; Pred. No. 1.3e-65;
Matches 277; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 4 GAGTCGTGGCCAGGACTGGTGAAGCCTGACAGACCCCTGTCCTGAGCTGGCTGTCTCT 63
Db 90 GAGTCGGGGCCAGGACTGGTGAAGCCTTTCAGAGACCCCTGTCCTGAGCTGTCTCT 149
QY 64 GCGGGCTCCATCCGAGTGGTGTACTACTGAGTGGATCGGCAACACCCAGGGAAG 123
Db 150 GGTGGCTCCATCCGAGTGGTGTACTACTGAGTGGATCGGCAACACCCAGGGAAG 209
QY 124 GCGCTGAGTGGATGGGTATCATCATCAGTGGGAAACACCTACAAACCCGTCCTC 183
Db 210 GCGCTGAGTGGATGGGTATCATCTTACAAATGGGTACCTACTACATCGTCCCTC 269
QY 184 AAGAGTCGAATGCCATGTCGGTAGACACGCTGTGAGAACAAAGTTCCTGAGGCTGAAC 243
Db 270 AAGAGTCGAGTTACCATATCTGTAGACACGCTCTCAGAACCAAGTTCCTGAGGCTGAGC 329
QY 244 TCTGTGACTCCGGGACACGCGGTGTATCTACTGCGAGGTAGATGGCTACACTTTG 303
Db 330 TCTGTGACTCCGGGACACGCGGTGTATCTACTGCGAAAGATCATCGAGCGACAGA 389
QY 304 GACATCTGGGCCAGGGAACCCCTGGTCACCGCTCTCCT 340
Db 390 GACGGGTACCAGCTGGGAATACCGAGGCTTTGACTACT 426

RESULT 11
US-08-360-125-9
; Sequence 9, Application US/08360125
; Patent No. 5767246
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Yoshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5767246ihiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,125
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; APPLICATION NUMBER:
```

```
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Creek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 366 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human antibody 1-3-1
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
; US-08-360-125-9

Query Match          69.3%; Score 237; DB 1; Length 366;
Best Local Similarity 82.3%; Pred. No. 1.3e-64;
Matches 289; Conservative 0; Mismatches 50; Indels 12; Gaps 1;

QY 4 GAGTCGTGGCCAGGACTGGTGAAGCCTGACAGACCCCTGTCCTGAGCTGGCTGTCTCT 63
Db 16 GAGTCGGGGCCAGGACTGGTGAAGCCTTTCGAGACCCCTGTCCTGAGCTGTCTCT 75
QY 64 GCGGGCTCCATCCGAGTGGTGTACTACTGAGTGGATCGGCAACACCCAGGGAAG 123
Db 76 GGTGGCTCCATCAGCAGTAGTAGTACTACTGCGGTGGATCGGCAACCCAGGGAAG 135
QY 124 GCGCTGAGTGGATGGGTATCATCTATCAGTGGGAAACACCTACAAACCCGTCCTC 183
Db 136 GGGCTGGAGTGGATGGGAGTAGTATCTATTATAGTGGGAGCACCTACTACAAACCCGTCCTC 195
QY 184 AAGAGTCGAATGGCATGTGCGTAGACACCTCTGAGAACAAAGTTCCTGAGGCTGAAC 243
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db	196	AAGAGTCGATCACCATATCCGTAGACACGTCCTCAAGACCGAGTTCCTCCCTGAAGCTGAGC	255
Qy	244	TCTGTGACTGCCGGCGAGACAGCGCCGTGTATTACTGTGCGA-----GGTTAGAT	291
Db	256	TCTGTGACCGCGGAGACACAGGCTGTATTACTGTGCGAGGGGAGCTACGGGGGCTAC	315
Qy	292	GGCTACACTTTGGACAICTGGGGCGCAGGGAACCCCTGGTCACCGTCTCTCTCA	342
Db	316	TACTACGGGTATGGACGCTCGGGGCGCAAGGGACCAAGCTCACCGTCTCTCTCA	366

RESULT 12

```

US-08-450-578-9
; Sequence 9, Application US/08450578
; Patent No. 5837845
;
; GENERAL INFORMATION:
;
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5837845hiiko ITO
; APPLICANT: Kazuhiro NAGAIKE
;
; TITLE OF INVENTION: Human Monoclonal Antibody
;
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
;
; TITLE OF INVENTION: Cell Membrane
;
; NUMBER OF SEQUENCES: 42
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSES: Wenderoth, Lind & Ponack
;
; STREET: 805 Fifteenth Street, N.W., #700
;
; CITY: Washington
;
; STATE: D.C.
;
; COUNTRY: U.S.A.
;
; ZIP: 20005

```

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/
/ 20000
/
/ COMPUTER READABLE FORM:
/
/ MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
/
/ COMPUTER: IBM Compatible
/
/ OPERATING SYSTEM: MS-DOS
/
/ SOFTWARE: WordPerfect 5.1
/
/ CURRENT APPLICATION DATA:
/
/ APPLICATION NUMBER: US/08/450,578
/
/ FILING DATE: May 25, 1995
/
/

```

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:

```

/ CELL LINE:
/ ORGANELLE:
/ IMMEDIATE SOURCE:
/ CLONING SOURCE:
/ LIBRARY:
/ CLONE:
/ POSITION IN GENOME:
/ CHROMOSOME/SEGMENT:
/ MAP POSITION:
/ UNITS:
/ FEATURE:
/ NAME/KEY:
/ LOCATION:
/ IDENTIFICATION METHOD:
/ OTHER INFORMATION:
/ PUBLICATION INFORMATION:
/ AUTHOR:
/ TITLE:
/ JOURNAL:
/ VOLUME:
/ ISSUE:
/ PAGES:
/ DATE:
/ DOCUMENT NUMBER:
/ FILING DATE:
/ PUBLICATION DATE:
/ RELEVANT RESIDUES IN SE
US-08-450-578-9

```

Query Match 69.3%; Score 237; DB 2; Length 366;

Qy	4	GAGTCTGGCCCAAGACTGTGTAAGCCTTGCACAGACCCCTGTCCTCAGCTGCCTCTCTCT	63
Db	16	GAGTCTGGCCCAAGACTGTGTAAGCCTTGGAGACCCCTGTCCTCAGCTGCCTCTCTCT	75
Qy	64	GGCGGCTCCATCCGAGTGGTGGTTACTACTGGAGTTGGATCCGGCAACACCCAGGGAAG	123
Db	76	GGTGGCTCCATCAGCAGTAGTAGTTACTCTGGGGCTGGATCCGGCAGCCGCCAGGGAAG	135
Qy	124	GGCCTGGAGTGGATTGGGTACATCTATCAGATGGGAACCTACAAACCCGTCCTC	183
Db	136	GGGCTGGAGTGGATTTGGGATGATCTATTATAGTGGGAGCACTACTACAACCCGTCCTC	195
Qy	184	AAGAGTCGAATTCGATGTCCGTAGACACAGTCTCAGAACAAAGTTCTCCCTCAGGCTGAAC	243
Db	196	AAGAGTCGAGTCCACCATATCCGTAGACACAGTCCAAAGAACAGTTCTCCCTGAGCTGAC	255
Qy	244	TCTGTGACTCCCGCGGACACGGCCGTGTATTACTGTGCGA-----GGTTAGAT	291
Db	256	TCGTGACCCGCGCAGACACGGCTGTGTATTACTGTGCGAGGGGAGCTACGGGGGCTAC	315
Qy	292	GGCTACACTTTTGACATCTCTGGGCGAGGGAACCCCTGGTCAACGCTCTCTCTCA	342
Db	316	TACTACGGTATGACCGTCTGGGGCCAAAGGGAACACGGTCAACGGCTCTCTCTCA	366

RESULT 13

US-09-017-628-9
Sequence 9, Application US/09017628
Patent No. 5990287
GENERAL INFORMATION:
APPLICANT: HOSOKAWA, Saiko
APPLICANT: TAGAWA, Toshiaki
APPLICANT: HIRAKAWA, Yoko
APPLICANT: ITO, No. 5990287hiko
APPLICANT: NAGAIKE, Kazuhiro
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
FILE REFERENCE: 177/527361KH
CURRENT APPLICATION NUMBER: US/09/017,628
CURRENT FILING DATE: 1998-03-02
EARLIER APPLICATION NUMBER: 08/360,125


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; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 9
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Hybridoma producing human antibody 1-3-1
US-09-017-628-9

Query Match          69.3%; Score 237; DB 2; Length 366;
Best Local Similarity 82.3%; Pred. No. 1.3e-64;
Matches 289; Conservative 0; Mismatches 50; Indels 12; Gaps 1;

QY 4 GAGTCTGCGCCAGGACTGGTGAAGCCTGCACAGACCCTGTCCTCAGCTGGCTGTCTCT 63
   |||||
Db 16 GAGTCGGGCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCTCAGCTGCACGTGTCTCT 75

QY 64 GCGGCTCCATCCCGAGTGGTGGTACTTACTGAGTGGATCCGCGAACACCCAGGGAAG 123
   |||||
Db 76 GGTGGCTCCATCAGCAGTAGTAGTACTTACTGCGGCTGGATCCGCCAGCCCCAGGGAAG 135

QY 124 GGCCTGAGTGGATTGGTGTACATCTACACAGTGGGAACCTCAACAACCCGTCCTC 183
   |||||
Db 136 GGGCTGGAGTGGATTGGAGTATCTATTATAGTGGAGCACCTACTACACCCGTCCTC 195

QY 184 AAGAGTCGAATTGCCATGTCGGTAGACACAGCTCTCAGAACAAAGTTCTCCCTGAGGCTGAAC 243
   |||||
Db 196 AAGAGTCGAGTCACCATATCCGTAGACAGTCCCAAGAACCAAGTTCTCCCTGAGGCTGAGC 255

QY 244 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGA-----GGTAGAT 291
   |||||
Db 256 TCTGTGACCGCGCAGACACGCGTGTATTACTGTGCGAGGGGAGCTACGGGGGCTAC 315

QY 292 GGCTACACTTTGGACATCTGGGGCCAGGAGACCCCTGTCACCGTCTCTCA 342
   |||||
Db 316 TACTACGGTATGGAGCTGTGGGGCCAGGAGCCACCGGTACCGTCTCTCA 366

RESULT 14
US-09-014-880-9
; Sequence 9, Application US/09014880
; Patent No. 5990297
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA et al.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
; TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., #800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/014,880
; FILING DATE: January 28, 1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/450,578
; FILING DATE: May 25, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
```

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; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-721-8200
; TELEFAX: 202-721-8250
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 366 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; CELL TYPE: Hybridoma producing human antibody 1-3-1
US-09-014-880-9

Query Match          69.3%; Score 237; DB 2; Length 366;
Best Local Similarity 82.3%; Pred. No. 1.3e-64;
Matches 289; Conservative 0; Mismatches 50; Indels 12; Gaps 1;

QY 4 GAGTCTGCGCCAGGACTGGTGAAGCCTGCACAGACCCTGTCCTCAGCTGGCTGTCTCT 63
   |||||
Db 16 GAGTCGGGCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCTCAGCTGCACGTGTCTCT 75

QY 64 GCGGCTCCATCCCGAGTGGTGGTACTTACTGAGTGGATCCGCGAACACCCAGGGAAG 123
   |||||
Db 76 GGTGGCTCCATCAGCAGTAGTAGTACTTACTGCGGCTGGATCCGCCAGCCCCAGGGAAG 135

QY 124 GGCCTGAGTGGATTGGTGTACATCTACACAGTGGGAACCTCAACAACCCGTCCTC 183
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QY 244 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGA-----GGTAGAT 291
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QY 292 GGCTACACTTTGGACATCTGGGGCCAGGAGACCCCTGTCACCGTCTCTCA 342
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RESULT 15
US-08-450-363-9
; Sequence 9, Application US/08450363
; Patent No. 6436434
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 6436434/hiho ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
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OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,363
FILING DATE: May 25, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLES:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:

US-08-450-363-9

Query Match 69.3%; Score 237; DB 4; Length 366;
Best Local Similarity 82.3%; Pred. No. 1.3e-64;
Matches 289; Conservative 0; Mismatches 50; Indels 12; Gaps 1;

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QY 64 GCGGCTCCATCCGCAGTCGTTGTTACTTACTGGAGTTGGATCGCCAAACACCCAGGGAAG 123
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QY 124 GGCCTGGAGTGGATTGGGTACATCTATCAAGTGGGAACACCTTACAACACCCGTCCTC 183
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DB 196 AAGAGTCGAGTCCCATATCCGTAGACACGTCGAAGAACAGTTCTCCCTGAAGCTGAGC 255
QY 244 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGGA-----GGTTAGAT 291
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QY 292 GGCTACACTTTGGACATCTGGGGCCAGGGAACCCCTGGTCACCGTCTCTCTCA 342
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Search completed: August 13, 2004, 07:18:06
Job time : 50.3636 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 12, 2004, 19:27:23 ; Search time 1471.46 Seconds
(without alignments)
10073.859 Million cell updates/sec

Title: US-10-027-725A-2

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Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	340.4	99.5	342	9	HSA458383 Homo sapi
2	324.4	94.9	342	9	HSA458384 Homo sapi
3	297.2	86.9	342	9	HSA458382 Homo sapi
4	275	80.4	432	9	HSA491911 Homo sapi
5	273.4	79.9	432	9	HSA491912 Homo sapi
6	271.8	79.5	354	9	HSA45064 Homo sapi
7	271.8	79.5	414	9	AF062112 Homo sapi
8	270.8	79.2	411	9	HST22X1
9	269	78.7	403	12	AF452917 Synthetic
10	268.6	78.5	351	9	HSA245020 Homo sapi
11	268.4	78.5	351	9	HSA244930 Homo sapi
12	268.4	78.5	358	9	AF021954 Homo sapi
13	268.4	78.5	360	6	AX061463 Sequence
14	267	78.1	360	9	HSU80129 Human immun
15	267	78.1	360	9	HSU80130 Human immun
16	266	77.8	354	9	HSA244955 Homo sapi
17	265.8	77.7	400	12	AF452909 Synthetic
18	265.6	77.7	357	9	HSA244949 Homo sapi
19	264.2	77.3	414	9	HST14X13
20	264.2	77.3	414	9	HST14X4
21	264	77.2	363	9	HSU80131 Human immun
22	263	76.9	412	12	AF452912 Synthetic
23	262.8	76.8	411	9	HST14X10
24	262.4	76.7	409	12	AF452947 Synthetic
25	262	76.6	357	9	HSA279523 Homo sapi
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38	257.8	75.4	366	9	HSU80111 Human immun
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40	257.8	75.4	414	9	HST14X15
41	257.8	75.4	414	9	HST14X5
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44	257.2	75.2	360	9	AB063905 Homo sapi
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ALIGNMENTS

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LOCUS HSA458383
DEFINITION Homo sapiens partial mRNA for immunoglobulin heavy chain variable region (IGHV gene), clone 60.
ACCESSION AJ458383.1 GI:20387065
VERSION IGHV gene; immunoglobulin heavy chain; variable region.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Flicker,S., Steinberger,P., Norderhaug,L., Sperr,W.R., Majlesi,Y., Valent,P., Kraft,D. and Valenta,R.

342 bp mRNA linear PRI 30-APR-2002
HSA458383
Homo sapiens partial mRNA for immunoglobulin heavy chain variable region (IGHV gene), clone 60.

Pred. No. is the number of results predicted by chance to have a

TITLE Conversion of grass allergen-specific human IgE into a protective
IgG1 antibody
Unpublished
JOURNAL
REFERENCE
AUTHORS Flicker S., Steinberger, P., Norderhaug, L., Sperr, W.R., Majlesi, Y.,
Valent, P., Kraft, D. and Valenta, R.
TITLE Conversion of grass allergen-specific human IgE into a protective
IgG1 antibody
JOURNAL
REFERENCE
AUTHORS Flicker, S.
TITLE Direct Submission
JOURNAL
REFERENCE
AUTHORS Flicker, S.
TITLE Submitted (24-APR-2002) Flicker S., Department of Pathophysiology,
General Hospital of Vienna, 30, Waehringer Guertel 18-20, A-1090
Vienna, AUSTRIA
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DB 241 ACCTCTGTACTGCCCGGACACCGCCGCTATTACTGTGCGGTCAGATGGGTACT 300
QY 301 TTGGCAACTGGGCGCAGGAACCCCTGGTCACCGTCTCTCA 342
DB 301 TTGGCAACTGGGCGCAGGAACCCCTGGTCACCGTCTCTCA 342
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HSA458384 342 bp mRNA linear PRI 30-APR-2002
LOCUS Homo sapiens partial mRNA for immunoglobulin heavy chain variable
region (IGHV gene), clone 100.
DEFINITION
AJ458384
ACCESSION
AJ458384.1 GI:20387067
VERSION
HSA458384.1
KEYWORDS
IGHV gene; immunoglobulin heavy chain; variable region.
SOURCE
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Flicker S., Steinberger, P., Norderhaug, L., Sperr, W.R., Majlesi, Y.,
Valent, P., Kraft, D. and Valenta, R.
Conversion of grass allergen-specific human IgE into a protective
IgG1 antibody
Unpublished
2 (bases 1 to 342)
Flicker, S.
Direct Submission
2 (bases 1 to 342)
Flicker, S.
Submitted (24-APR-2002) Flicker S., Department of Pathophysiology,
General Hospital of Vienna, 30, Waehringer Guertel 18-20, A-1090
Vienna, AUSTRIA
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Best Local Similarity 96.8%; Pred. No. 6.9e-85;
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DB 181 CTCAGAGTCGAATTACCATGTAGTACAGCTCTAAGAACCACTTCTCCCTGAGACTG 240
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QY 301 TTGGCAACTGGGCGCAGGAACCCCTGGTCACCGTCTCTCA 342
DB 301 TTGGCAACTGGGCGCAGGAACCCCTGGTCACCGTCTCTCA 342
RESULT 3
HSA458382 342 bp mRNA linear PRI 30-APR-2002
LOCUS Homo sapiens partial mRNA for immunoglobulin heavy chain variable
region (IGHV gene), clone 94.
DEFINITION
AJ458382
ACCESSION
AJ458382.1 GI:20387063
VERSION

KEYWORDS	IGHV gene; immunoglobulin heavy chain; variable region.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 Flicker, S., Steinberger, P., Norderhaug, L., Sperr, W.R., Majlesi, Y., Valent, P., Kraft, D. and Valenta, R.
TITLE	Conversion of grass allergen-specific human IgE into a protective IgG1 antibody
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 342)
AUTHORS	Flicker, S.
TITLE	Direct Submission
JOURNAL	Submitted (24-APR-2002) Flicker S., Department of Pathophysiology, General Hospital of Vienna, 30, Maehringerguertel 18-20, A-1090 Vienna, AUSTRIA
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Db	301 TTGACATCTGGGCGCAGGGAACCTGGTCACCGTCTCCTCA 342
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LOCUS	
DEFINITION	Homo sapiens mRNA for immunoglobulin heavy chain V-D-J-Ce region (Clone HD17 C9).
ACCESSION	AJ491911
VERSION	AJ491911.1 GI:24415808
KEYWORDS	constant region; epsilon chain; IGH gene; immunoglobulin heavy chain; variable region.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	1 Coker, H.A., Durham, S.R. and Gould, H.J.
AUTHORS	Local somatic hypermutation and class switch recombination in the nasal mucosa of allergic rhinitis patients
TITLE	J. Immunol. 171 (10), 5602-5610 (2003)
JOURNAL	22970235
MEDLINE	14607969
REFERENCE	2 (bases 1 to 432)
AUTHORS	Coker, H.A.
TITLE	Direct Submission
JOURNAL	Submitted (26-JUN-2002) Coker H.A., Biomedical Sciences, Randall Centre, King's College London, Guy's Campus, London, SE1 1UL, UNITED KINGDOM
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JOURNAL REFERENCE
2 (bases 1 to 354)
Dono, M.
Direct Submission
Submitted (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca
sul Cancro, Immunologia Clinica, L.go Rosanna benzi 10- Genova,
ITALY
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Qy 184 AAGAGTCGAATTACCATGTCAGTGAACACCTTCTCCCTGAGACTGACC 243
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Qy 196 AAGAGTCGAATTACCATGTCAGTGAACACCTTCTCCCTGAGACTGACC 255
Db |||||
Qy 244 TCTGTGACTCGCGGAGACCGCGCTTATTACTGTGCGCGTTCAGATGGGTATCTTTG 303
Db |||||
Qy 256 TCTGTGACTCGCGGAGACCGCGCTTATTACTGTGCGCGGATAGTACTACTTT 315
Db |||||
Qy 304 GACAACTGGGCGGAGGACCTGGTACACCTCTCTCTCA 342
Db |||||
Qy 316 GACTACTGGGCGGAGGACCTGGTACACCTCTCTCTCA 354
Db |||||
RESULT 7
AF062112
LOCUS AF062112
DEFINITION Homo sapiens clone 21u-26 immunoglobulin heavy chain variable
region (IGH) mRNA, partial cds.
ACCESSION AF062112
VERSION AF062112.1 GI:3170686
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 414)
Wang, X. and Stollar, B.D.
Immunoglobulin VH gene expression in human aging
Clin. Immunol. 93 (2), 132-142 (1999)
99459182
PUBMED 10527689
2 (bases 1 to 414)
Wang, X. and Stollar, B.D.
Direct Submission
AUTHORS Wang, X. and Stollar, B.D.
TITLE Immunoglobulin VH gene expression in human aging
JOURNAL Clin. Immunol. 93 (2), 132-142 (1999)
FEATURES
Location/Qualifiers
1..414
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="14"
/map="14q32.33"
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/notes="from elderly repertoire 21u"
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/product="immunoglobulin heavy chain variable region"
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/db_xref="GI:3170687"
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/sig_peptide
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58..>414
V_region
/gene="IGH"
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Query Match 79.5%; Score 271.8; DB 9; Length 414;
Best Local Similarity 87.6%; Pred. No. 2.6e-69;
Matches 297; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
Qy 4 GAGTCTGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGACACTGTCTCT 63
Db |||||
Qy 73 GAGTCGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGACACTGTCTCT 132
Db |||||
Qy 64 GGTGGCTCCATCCGAGTGGTGGTATTATTGGAGTTGGGTTCGCGCACCTCCAGGGAAG 123
Db |||||
Qy 133 GGTGGCTCCATCAGCAGTGGTGGTATTACTTGGAGTTGGATCCGCGACCCCGAGGGAAG 192
Db |||||
Qy 124 GGCTTGGAGTGGATCGGCAACATCTATCAGTGGCAACACCTTCTCCCTGAGACTGACC 183
Db |||||
Qy 193 GGCTTGGAGTGGATCGGCAACATCTATCAGTGGCAACACCTTCTCCCTGAGACTGACC 252
Db |||||
Qy 184 AAGAGTCGAATTACCATGTCAGTGAACACCTTCTCCCTGAGACTGACC 243
Db |||||
Qy 253 AAGAGTCGAATTACCATGTCAGTGAACACCTTCTCCCTGAGACTGACC 312
Db |||||
Qy 244 TCTGTGACTCGCGGAGACCGCGCTTATTACTGTGCGCGTTCAGATGGGTATCTTTG 303
Db |||||
Qy 313 TCTGTGACTCGCGGAGACCGCGCTTATTACTGTGCGCGTTCAGATGGGTATCTTTG 372
Db |||||
Qy 304 GACAACTGGGCGGAGGAAACCTGGTCAACCTCTCTCTCA 342
Db |||||
Qy 373 GACTACTGGGCGGAGGAAACCTGGTCAACCTCTCTCTCA 411
Db |||||
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RESULT 8
LOCUS      HST22X1
DEFINITION H sapiens mRNA for Ig heavy chain variable region (VH4DJ) (clone
            T22.1).
ACCESSION  Z75385.1 GI:2062048
VERSION    1
KEYWORDS   immunoglobulin; immunoglobulin heavy chain; immunoglobulin
            superfamily; variable region.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 411)
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS    Tonnelie,C., D'Ercole,C., Depraetere,V., Metras,D., Boubli,L. and
            Fougereau,M.
TITLE      Human thymic B cells largely overexpress the VH4 Ig gene family. A
            possible role in the control of tolerance in situ?
JOURNAL    Int. Immunol. 9 (3), 407-414 (1997)
MEDLINE    97244170
PUBMED     9089979
REFERENCE  2 (bases 1 to 411)
            Tonnelie,C.
AUTHORS    Direct Submission
TITLE      Submitted (26-JUN-1996) Cecile Tonnelie, Centre d'Immunologie
            Marseille Luminy, Marseille, 13288, France
JOURNAL    Marseille Luminy, Marseille, 13288, France
FEATURES   source
            Location/Qualifiers
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                /db_xref="taxon:9606"
                /chromosome="14"
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                /tissue_type="thymus"
                /clone_lib="T22"
                /dev_stage="infant"
            V_region
            1..411
                /product="Ig heavy chain variable region (VH4DJ)"
            sig_peptide
            1..57
            V_segment
            58..354
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            D_segment
            355..377
            J_segment
            378..411
ORIGIN
Query Match      79.2%; Score 270.8; DB 9; Length 411;
Best Local Similarity 87.6%; Pred. No. 5.1e-69;
Matches 296; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
QY      4  GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACCTGTCTCT 63
DB      73  GAGTCGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACCTGTCTCT 132
QY      64  GGTGGCTCCATCCGACGTGGTGGTTATTATTGGAGTTGGGTGGCGCAGCCTCCAGGGAAG 123
DB      133  GGTGGCTCCATCAGCAGTGGTGGTTACTACTGGAGTGGATCCGCTGCACCCAGGAAG 192
QY      124  GGCCTGGAGTGCAGGCAACATCTATCAGTGGCAACACCTACACCAACCCGTCCTC 183
DB      193  GGCCTGGAGTGGGTGGTACATCTATTACGTGGGAGCACCTACTACACCCGTCCTC 252
QY      184  AAGAGTCGAATTACCATGTCACTAGACACGTCTAAGAACCACTTCTCCCTGAGACTGACC 243
DB      253  AAGAGTCGAGTTACCATATCAGTAGACACGCCTAAGAACCACTTCTCCCTGAAGCTGAGC 312
QY      244  TCTGTGACTGCCCGGACACGGCCCTCTATTACTGTGGCGGTGCAGATGGGTATTACTTTG 303
DB      313  TCTGTGACTGCCCGGACACGGCCGCTATTACTGTGGAGAGTGGGTTATTGTGTAGTAGT 372
QY      304  GACAACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCCTC 341
DB      373  TCCAGTGGGGCCAGGGAACCCCTGGTCAACCGTCTCCTC 410
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```
RESULT 9
LOCUS      AF452917
DEFINITION Synthetic construct clone 7-161VH rotavirus VP7-specific antibody
            heavy chain variable region mRNA, partial sequence.
ACCESSION  AF452917
VERSION    1
KEYWORDS   synthetic construct
            synthetic construct
            artificial sequences.
SOURCE     AF452917.1 GI:25988060
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 403)
            Weitkamp,J.-H. and Crowe,J.E. Jr.
            Infant B Cell Repertoires are Sufficiently Diversified for Mature
            Virus-Specific Responses, but Lack Somatic Mutations
            Unpublished
            2 (bases 1 to 403)
            Weitkamp,J.-H. and Crowe,J.E. Jr.
            Direct Submission
            Submitted (28-NOV-2001) Pediatrics, Vanderbilt University Medical
            Center, 1161 21st Avenue South, D-7235 Medical Center North,
            Nashville, TN 37232-2581, USA
JOURNAL    Location/Qualifiers
FEATURES   source
            Location/Qualifiers
            1..403
                /organism="synthetic construct"
                /mol_type="mRNA"
                /db_xref="taxon:32630"
                /clone="7-161VH"
                /note="includes synthetic primer used to amplify the
                sequence from Homo sapiens mRNA"
            misc_feature
            1..>403
                /note="rotavirus VP7-specific antibody heavy chain
                variable region"
ORIGIN
Query Match      78.7%; Score 269; DB 12; Length 403;
Best Local Similarity 88.9%; Pred. No. 1.7e-68;
Matches 303; Conservative 0; Mismatches 35; Indels 3; Gaps 1;
QY      5  AGTCGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACCTGTCTCTG 64
DB      42  AGTCGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACCTGTCTCTG 101
QY      65  GTGGCTCCATCGCAGTGGTGGTTATTATTGGAGTTGGTCCGCCAGCCTCCAGGAAG 124
DB      102  GTGGCTCCATCAGCAGTGGTGGTTACTACTGGAGTGGATCGCCAGCACCCAGGAAG 161
QY      125  GCCTGGAGTGGATCGGCAACATCTATCAGTGGCAACACCTTACCAACACCCGTCCTCA 184
DB      162  GCCTGGAGTGGATTGGGTACATCTATTACAGTGGGAGCACCTTACTACAACCCGTCCTCA 221
QY      185  AGAGTCGAATTACCAATGTCAGTAGACAGCTTAAGAACCACTTCTCCCTGAGACTGACCT 244
DB      222  AGAGTCGAGTTACCATATCAGTAGACAGCTTAAGAACCACTTCTCCCTGAGACTGAGCT 281
QY      245  CTGTCACTGCCCGGACACGCGCTCTATTACTGTGGG---CGGTCAAGATGGGTATCTT 301
DB      282  CTGTCACTGCCCGGACACGCGCTGTATTACTGTGGGAGAGGTGGGTACGGCTGACT 341
QY      302  TGGACAACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA 342
DB      342  TTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA 382
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RESULT 10
LOCUS      HSA245020
DEFINITION Homo sapiens mRNA for immunoglobulin mu heavy chain variable
            region, partial, clone 2-B66.
ACCESSION  AJ245020
VERSION    1
KEYWORDS   HSA245020
            Homo sapiens mRNA for immunoglobulin mu heavy chain variable
            region, partial, clone 2-B66.
SOURCE     AJ245020.1 GI:4995498
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KEYWORDS IGM; IgM heavy chain; immunoglobulin mu heavy chain; variable region

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 Dono, M., Zupo, S., Leanza, N., Melioli, G., Fogli, M., Melagrana, A., Chiorazzi, N. and Ferrarini, M.

TITLE Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic marginal zone equivalents

JOURNAL J. Immunol. 164 (11), 5596-5604 (2000)

MEDLINE 20281644

PUBMED 10820234

REFERENCE 2 (bases 1 to 351)

AUTHORS Dono, M.

TITLE Direct Submission

JOURNAL Submitted (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca sul Cancro, Immunologia Clinica, L.go Rosanna Benzi 10- Genova, ITALY

FEATURES

source Location/Qualifiers

1..351

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/chromosome="14"

/clone="2-E66"

/cell_type="B-lymphocyte"

/tissue_type="tonsil"

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gene 1..351

/gene="IGHV4-30-4"

CDS <1..>351

/gene="IGHV4-30-4"

/codon_start=1

/product="immunoglobulin mu heavy chain variable region"

/protein_id="CAB44154.1"

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/translation="QVQLQESGPGLVKPSQTLSTCTVSGSISGGYYSWIRQPPG KLEWIGIYYSGTYSNPISLKSRTISVDTSKNQFSLKLSVTAADTAVYVCARGW SVDYWGQGTLVTVSS"

V_region <1..>351

/gene="IGHV4-30-4"

/product="immunoglobulin mu heavy chain variable region"

ORIGIN

Query Match 78.5%; Score 268.6; DB 9; Length 351;

Best Local Similarity 89.1%; Pred. No. 2.2e-68;

Matches 302; Conservative 0; Mismatches 34; Indels 3; Gaps 1;

QY 4 GAGTCTGCCCCAGGACTGGTGAAGCTTCACAGACCCCTGTCCTCACCTGCACCTGTCTCT 63

Db 16 GAGTCGGGCCAGGACTGGTGAAGCTTCACAGACCCCTGTCCTCACCTGCACCTGTCTCT 75

QY 64 GGTGGCTCCATCCGAGTGGTGGTTATTATTGGAGTTGGTCCGCCAGCTCCAGGGAAG 123

Db 76 GGTGGCTCCATCAGACAGTGGTGGTTATTATTGGAGTTGGTCCGCCAGCTCCAGGGAAG 135

QY 124 GGCTCGAGTGGATCGGCACCATCTATCAGAGTGGCAACACCTACACAAACCCGTCCTC 183

Db 136 GGCTCGAGTGGATCGGCACCATCTATCAGAGTGGCAACACCTACACAAACCCGTCCTC 195

QY 184 AAGAGTCGAATTACCATGTCAGTAGACACGCTCTAAGAACCATCTCTCCCTGAGCTGACC 243

Db 196 AAGAGTCGAGTTACCATGTCAGTAGACACGCTCTAAGAACCATCTCTCCCTGAGCTGAGC 255

QY 244 TCTGTACTCGCGGACACGCGCTCTATTACTGTGCGCGGTGAGTGGTATCTTGG 303

Db 256 TCTGTACTCGCGGACACGCGCTGTTACTGTGCGCGTATCTTGGTGGTGGTGGTGGTGGT 312

QY 304 GACAACTGGGGCCAGGGAACCTGGTCAACCCCTCTCCTCA 342

Db 313 GACTACTGGGCCAGGGAACCTGGTCAACCCCTGTCACCTCTCCTCA 351

RESULT 11

HSA244930 351 bp mRNA linear PRI 01-JUN-2000

LOCUS HSA244930

DEFINITION Homo sapiens mRNA for immunoglobulin mu heavy chain variable region, partial, clone 1-A34.

ACCESSION AJ244930

VERSION AJ244930.1 GI:4995319

KEYWORDS IGM; IgM heavy chain; immunoglobulin mu heavy chain; variable region.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 Dono, M., Zupo, S., Leanza, N., Melioli, G., Fogli, M., Melagrana, A., Chiorazzi, N. and Ferrarini, M.

TITLE Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic marginal zone equivalents

JOURNAL J. Immunol. 164 (11), 5596-5604 (2000)

MEDLINE 20281644

PUBMED 10820234

REFERENCE 2 (bases 1 to 351)

AUTHORS Dono, M.

TITLE Direct Submission

JOURNAL Submitted (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca sul Cancro, Immunologia Clinica, L.go Rosanna Benzi 10- Genova, ITALY

FEATURES

source Location/Qualifiers

1..351

/organism="Homo sapiens"

/mol_type="mRNA"

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/chromosome="14"

/clone="1-A34"

/cell_type="B-lymphocyte"

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CDS <1..>351

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/db_xref="REMTREMBL.CAB44065"

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V_region <1..>351

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Query Match 78.5%; Score 268.4; DB 9; Length 351;

Best Local Similarity 88.6%; Pred. No. 2.6e-68;

Matches 303; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

QY 4 GAGTCTGCCCCAGGACTGGTGAAGCTTCACAGACCCCTGTCCTCACCTGCACCTGTCTCT 63

Db 10 GAGTCGGGCCAGGACTGGTGAAGCTTCACAGACCCCTGTCCTCACCTGCACCTGTCTCT 69

QY 64 GGTGGCTCCATCCGAGTGGTGGTTATTATTGGAGTTGGTCCGCCAGCTCCAGGGAAG 123

Db 70 GGTGGCTCCATCAGACAGTGGTGGTTATTATTGGAGTTGGTCCGCCAGCTCCAGGGAAG 129

QY 124 GGCTCGAGTGGATCGGCACCATCTATCAGAGTGGCAACACCTACACAAACCCGTCCTC 183

Db 130 GGCTCGAGTGGATCGGCACCATCTATCAGAGTGGGAGCACCTACTACAAACCCGTCCTC 189

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QY 184 AAGAGTCGAATTACCATGTCTAGACACGCTCTAAGAACCACTTCTCCCTGAGACTGACC 243
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Db 190 AAGAGTCGAGTTACCATATCACTAGACACGCTCTAAGAACCACTTCTCCCTGAGCTGAGC 249
    |||
QY 244 TCTGTGACTGCGCGGACACGCGCGCTCTATTACTGTGGG---CGGTGAGATGGGTATCT 300
    |||
Db 250 TCTGTGACTGCGCGGACACGCGCGCTGTATTACTGTGCGAGAGGCAAGAGAGACTTCTAC 309
    |||
QY 301 TTGGACAACTGGGCGCAGGGAACCTGTGTCACCGTCTCTCTCA 342
    |||
Db 310 TTTGACTACTGGGGCCAGGGAACCTGTGTCACCGTCTCTCTCA 351
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RESULT 12
LOCUS AF021954 358 bp mRNA linear PRI 02-APR-1998
DEFINITION Homo sapiens ID:CLL019 IgM heavy chain variable region mRNA,
ACCESSION AF021954 partial cds.
VERSION AF021954.1 GI:3004697
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Differences in Ig variable region gene use and mutation in IgM vs
IgG CLL suggest selection for distinct surface membrane Ig
receptors
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 358)
AUTHORS Chiorazzi, N.
TITLE Direct Submission
JOURNAL Submitted (02-SEP-1997) Medicine, North Shore University Hospital,
350 Community Drive, Manhasset, NY 11030, USA
FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="14"
/clone="ID:CLL019"
/cell_type="B lymphocyte"
<1..>358
/codon_start=1
/product="IgM heavy chain variable region"
/protein_id="AAC09088.1"
/db_xref="GI:3004698"
/translation="QVQLQESGFLVKPSQTLISLCTVSGGSISSGGYVWSWIRHPG
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CDS
ORIGIN
Query Match 78.5%; Score 268.4; DB 9; Length 358;
Best Local Similarity 88.6%; Pred. No. 2.6e-68;
Matches 303; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

QY 4 GAGTCGCGCCAGGACTGTGAGCCTTCACAGACCTCTCCCTCACCTGCACTGTCTCT 63
    |||
Db 16 GAGTCGCGCCAGGACTGTGAGCCTTCACAGACCTCTCCCTCACCTGCACTGTCTCT 75
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QY 64 GTTGGCTCCATCCGACGCTGTGTTATTATTGGAGTTGGGTCCGCGAGCTCCAGGGAAG 123
    |||
Db 76 GTTGGCTCCATCAGCAGTGGTGTGTTACTACTGGAGCTGGATCCGCGACCAACCCAGGGAAG 135
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QY 124 GGCCTGGAGTGATCGGCAACATCTATCACAGTGGCAACACCTACAAACCCGTCCTC 183
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Db 136 GGCCTGGAGTGATGGGTGACATCTATTACAGTGGGAGCACCTACTACAAACCCGTCCTC 195
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QY 184 AAGAGTCGAATTACCATGTCTAGACACGCTCTAAGAACCACTTCTCCCTGAGACTGACC 243
    |||
Db 196 AAGAGTCGAGTTACCATATCAGTAGACACGCTCTAAGAACCACTTCTCCCTGAGCTGAGC 255
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Query Match 78.5%; Score 268.4; DB 9; Length 358;
Best Local Similarity 88.6%; Pred. No. 2.6e-68;
Matches 303; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

QY 4 GAGTCGCGCCAGGACTGTGAGCCTTCACAGACCTCTCCCTCACCTGCACTGTCTCT 63
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Db 19 GAGTCGCGCCAGGACTGTGAGCCTTCACAGACCTCTCCCTCACCTGCACTGTCTCT 78
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QY 64 GTTGGCTCCATCCGACGCTGTGTTATTATTGGAGTTGGGTCCGCGAGCTCCAGGGAAG 123
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Db 79 GTTGGCTCCATCAGCAGTGGTGTGTTACTACTGGAGCTGGATCCGCGACCAACCCAGGGAAG 138
    |||

QY 124 GGCCTGGAGTGATCGGCAACATCTATCACAGTGGCAACACCTACAAACCCGTCCTC 183
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Db 139 GGCCTGGAGTGATGGGTGACATCTATTACAGTGGGAGCACCTACTACAAACCCGTCCTC 198
    |||

QY 184 AAGAGTCGAATTACCATGTCTAGACACGCTCTAAGAACCACTTCTCCCTGAGACTGACC 243
    |||
Db 199 AAGAGTCGAGTTACCATATCAGTAGACACGCTCTAAGAACCACTTCTCCCTGAGCTGAGC 258
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QY 244 TCTGTGACTGCGCGGACACGCGCGCTCTATTACTGTGGG---CGGTGAGATGGGTATCT 300
    |||
Db 259 TCTGTGACTGCGCGGACACGCGCGCTGTATTACTGTGCGAGAGGGGTAGTAGTGAGCTGG 318
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QY 301 TTGGACAACTGGGCGCAGGGAACCTGTGTCACCGTCTCTCTCA 342
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Db 319 TTCGACCCCTGGGGCCAGGGAACCTGTGTCACCGTCTCTCTCA 360
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RESULT 14
LOCUS HSU0129 360 bp DNA linear PRI 19-FEB-1997
DEFINITION Human immunoglobulin heavy chain variable region (V4-31) gene,
partial cds.
ACCESSION HSU0129
VERSION U80129.1 GI:1791100
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
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QY 244 TCTGTGACTGCGCGGACACGCGCGCTCTATTACTGTGGCGGTCTAGATGGGTATAC---T 300
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Db 256 TCTGTGACTGCGCGGACACGCGCGCTGTATTACTGTGCAAGGGAGCTACGCTGACCCAC 315
    |||

QY 301 TTGGACAACTGGGCGCAGGGAACCTGTGTCACCGTCTCTCTCA 342
    |||
Db 316 TTTGACTACTGGGGCCAGGGAACCTGTGTCACCGTCTCTCTCA 357
    |||

RESULT 13
LOCUS AX061463 360 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 32 from Patent WO0100678.
ACCESSION AX061463
VERSION AX061463.1 GI:12406598
KEYWORDS Human immunodeficiency virus 1 (HIV-1)
SOURCE Human immunodeficiency virus 1
ORGANISM Viruses; Retroviridae; Lentivirus; Primate
          lentivirus group.
REFERENCE
AUTHORS Watkins, B.A. and Reitz, M.S.
TITLE Human monoclonal antibodies to hiv-1 envelope glycoprotein gp120
JOURNAL Patent: WO 0100678-A 32 04-JAN-2001;
          THE GOVERNMENT OF THE UNITED STATES OF AMERICA (US)
FEATURES
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/organism="Human immunodeficiency virus 1"
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/note="VH"

ORIGIN
Query Match 78.5%; Score 268.4; DB 6; Length 360;
Best Local Similarity 88.6%; Pred. No. 2.6e-68;
Matches 303; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

QY 4 GAGTCGCGCCAGGACTGTGAGCCTTCACAGACCTCTCCCTCACCTGCACTGTCTCT 63
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Db 19 GAGTCGCGCCAGGACTGTGAGCCTTCACAGACCTCTCCCTCACCTGCACTGTCTCT 78
    |||

QY 64 GTTGGCTCCATCCGACGCTGTGTTATTATTGGAGTTGGGTCCGCGAGCTCCAGGGAAG 123
    |||
Db 79 GTTGGCTCCATCAGCAGTGGTGTGTTACTACTGGAGCTGGATCCGCGACCAACCCAGGGAAG 138
    |||

QY 124 GGCCTGGAGTGATCGGCAACATCTATCACAGTGGCAACACCTACAAACCCGTCCTC 183
    |||
Db 139 GGCCTGGAGTGATGGGTGACATCTATTACAGTGGGAGCACCTACTACAAACCCGTCCTC 198
    |||

QY 184 AAGAGTCGAATTACCATGTCTAGACACGCTCTAAGAACCACTTCTCCCTGAGACTGACC 243
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Db 199 AAGAGTCGAGTTACCATATCAGTAGACACGCTCTAAGAACCACTTCTCCCTGAGCTGAGC 258
    |||

QY 244 TCTGTGACTGCGCGGACACGCGCGCTCTATTACTGTGGG---CGGTGAGATGGGTATCT 300
    |||
Db 259 TCTGTGACTGCGCGGACACGCGCGCTGTATTACTGTGCGAGAGGGGTAGTAGTGAGCTGG 318
    |||

QY 301 TTGGACAACTGGGCGCAGGGAACCTGTGTCACCGTCTCTCTCA 342
    |||
Db 319 TTCGACCCCTGGGGCCAGGGAACCTGTGTCACCGTCTCTCTCA 360
    |||

RESULT 14
LOCUS HSU0129 360 bp DNA linear PRI 19-FEB-1997
DEFINITION Human immunoglobulin heavy chain variable region (V4-31) gene,
partial cds.
ACCESSION HSU0129
VERSION U80129.1 GI:1791100
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 360)
 Analysis of rearranged immunoglobulin heavy chain variable region
 genes obtained from a bone marrow transplant (BMT) recipient
 Clin. Exp. Immunol. 107 (2), 372-380 (1997)
 JOURNAL
 MEDLINE
 PUBMED
 97182739
 9030878
 REFERENCE
 2 (bases 1 to 360)
 Glas,A.M., Nottenburg,C. and Milner,E.C.B.
 Direct Submission
 TITLE
 Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center,
 JOURNAL
 1000 Seneca Street, Seattle, WA 98101, USA
 FEATURES
 Location/Qualifiers
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gene

CDS

ORIGIN

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 Best Local Similarity 88.1%; Pred. No. 6.7e-68;
 Matches 304; Conservative 0; Mismatches 35; Indels 6; Gaps 1;
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 16 GAGTCGGGCCAGACTGGTGAAGCCTTACAGACCCCTGTCCTCAGCTGCTCT 75
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 64 GGTGGCTCCATCCGACGTGGTGTATATTGGAGTTGGTCCGCCAGCCTCCAGGGAAG 123
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 76 GGTGGCTCCATCAGCAGTGGTGTATTCTAGGAGCTGGATCCGCCAGCACCAGGGAAG 135
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 124 GGCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTACAAACCCGTCCTC 183
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 184 AAGAGTCGAATTACCATGTGAGTAGACAGTCTTAAGAACACATTTCTCCCTGAGACTGACC 243
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 256 TCTGTGACTGCCGGGACAGCGCGTGTATTACTGTGCGAGAGGGGTGAGTGGGTGGTAC 315
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 298 ACTTTGGACAACTGGGGCCAGGGAACCTGGTCAACCGTCTCTCA 342
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 316 TATTTTGACTACTGGGGCCAGGGAACCTGGTCAACCGTCTCTCA 360
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RESULT 15

HSU80130

LOCUS

HSU80130 360 bp DNA linear PRI 19-FEB-1997

Human immunoglobulin heavy chain variable region (V4-31) gene,
 partial cds.
 U80130
 U80130.1 GI:1791102
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 360)
 Analysis of rearranged immunoglobulin heavy chain variable region
 genes obtained from a bone marrow transplant (BMT) recipient
 Clin. Exp. Immunol. 107 (2), 372-380 (1997)
 JOURNAL
 MEDLINE
 PUBMED
 97182739
 9030878
 REFERENCE
 2 (bases 1 to 360)
 Glas,A.M., Nottenburg,C. and Milner,E.C.B.
 Direct Submission
 TITLE
 Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center,
 JOURNAL
 1000 Seneca Street, Seattle, WA 98101, USA
 FEATURES
 Location/Qualifiers
 source
 1. .360
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
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 /clone="3f1e2"
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 /note="CD19+ peripheral blood B cells obtained from a bone
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 55 in reference 1"
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Query Match 78.1%; Score 267; DB 9; Length 360;
 Best Local Similarity 88.1%; Pred. No. 6.7e-68;
 Matches 304; Conservative 0; Mismatches 35; Indels 6; Gaps 1;
 4 GAGTCTGGCCAGACTGGTGAAGCCTTACAGACCCCTGTCCTCAGCTGCTCT 63
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 16 GAGTCGGGCCAGACTGGTGAAGCCTTACAGACCCCTGTCCTCAGCTGCTCT 75
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 64 GGTGGCTCCATCCGACGTGGTGTATATTGGAGTTGGTCCGCCAGCCTCCAGGGAAG 123
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 196 AAGAGTCGAGTTACCATGTAGTAGACAGTCTTAAGAACACATTTCTCCCTGAGACTGAGC 255
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Db 316 TATTTGACTACTGGGGCCAGGGAAACCCCTGGTCAACCGTCTCTCA 360

Search completed: August 13, 2004, 03:57:59
Job time : 1472.46 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 00:12:28 ; Search time 2005.71 Seconds

(without alignments)
5091.898 Million cell updates/sec

Title: US-10-027-725A-2

Perfect score: 342

Sequence: 1 ctccagctgcccaggact.....ccctgggtcacggtctctctca 342

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

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27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	263.8	77.1	832	9	AUI22174
2	250.8	73.3	509	10	AW406349
3	250.2	73.2	369	10	AW404242
4	250.2	73.2	677	12	BG686767

5	249.6	73.0	607	12	BM783015
6	248.2	72.6	490	14	CD689564
7	241.4	70.6	725	12	BG431274
8	241.2	70.5	643	9	AUI34293
9	240	70.2	904	13	BQ710488
10	239.8	70.1	959	13	BU899307
11	238.8	69.8	890	13	EX324929
12	238.2	69.6	903	13	BQ706579
13	238.2	69.6	1108	12	BM920469
14	237.2	69.4	977	13	EX336901
15	237.2	69.4	1201	13	EX336959
16	237	69.3	914	12	BG757054
17	237	69.3	939	13	BQ708070
18	236.4	69.1	828	10	BF974568
19	236.2	69.1	1050	9	AL552672
20	236.2	68.8	447	10	AW402200
21	234.8	68.7	596	12	BM817833
22	234.8	68.7	813	13	BQ710364
23	234.6	68.6	582	10	AW401348
24	234.6	68.6	814	12	BG685325
25	233.6	68.3	1019	13	BQ072420
26	233.6	68.3	1195	13	BQ707644
27	233.4	68.2	474	10	AW408410
28	233.4	68.2	915	13	BQ706358
29	233.2	68.2	658	13	EX505812
30	233	68.1	1201	13	EX380759
31	232.8	68.1	421	10	AW407630
32	232	67.8	363	10	AW403420
33	232	67.8	915	13	BQ711871
34	232	67.8	923	13	BQ707945
35	232	67.8	928	13	BQ707875
36	232	67.8	959	13	BQ709473
37	231.8	67.7	924	13	BQ708516
38	231.6	67.7	924	12	BG758027
39	231.6	67.7	987	13	BQ707970
40	231.4	67.7	650	12	BG684403
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42	231.4	67.7	929	12	BG341823
43	231	67.5	524	13	BU429270
44	231	67.5	856	13	BQ421299
45	230.6	67.4	661	12	BG686421

ALIGNMENTS

RESULT 1
AUI22174

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AUI22174 MAMMAL Homo sapiens CDNA clone MAMMAL001802 5', mRNA linear EST 01-AUG-2002 sequence.

AUI22174.1 GI:10937409

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,

Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and

Isogai,T.

HRI human cDNA project

Unpublished (2000)

Contact: Takao Isogai

Genomics Laboratory

Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix

Research Institute; cDNA library construction: Department of

Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

FEATURES

source

Location/Qualifiers

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/clone="MAMMAL001802"
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/clone_lib="MAMMAL"
/note="Vector: pME18SFL3"

ORIGIN

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Best Local Similarity 86.1%; Pred. No. 5.8e-58;
Matches 292; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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DB 110 GAGTGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACCTGCTCT 169

QY 64 GTGTGCTCCATCCGACGAGTGGTGGTATTATTGGAGTTGGTGGCCAGCCTCCAGGAG 123
DB 170 GGTGGCTCCATCAGCAGTGGTGAAGCCTACTGGAGTTGGATCGCCAGCCCCCAGGAG 229

QY 124 GGCCTGGAGTGATCGGCAACATCTATCACAGTGGCAACACCTACAAACCCGTCCTC 183
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DB 290 AAGATCGAGTTACCATATCAACAGACATGTCCAAGACGAGTTCTCCCTGAAGCTAAC 349

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QY 304 GACAACTGGGGCCAGGAAACCTTGTCACCGTCTCTCTCA 342
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RESULT 2

AW406349

LOCUS

AW406349 509 bp mRNA linear EST 16-FEB-2000
UI-HF-BL0-aco-h-03-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3059933 5', mRNA sequence.

ACCESSION

AW406349

VERSION

AW406349.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 509)

AUTHORS

NIH-MGC http://mgc.nci.nih.gov/.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

cDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: M13 Forward.

FEATURES

source

Location/Qualifiers

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/lab_host="DH10B (lTI)"

/clone_lib="NIH_MGC_37"

/note="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI;

Constructed from size fractionated cytoplasmic mRNA

(1.5-2.5kb). Directionally cloned. Cells provided by Louis

M. Staudt, Ph.D. Library preparation by Maria de Fatima

Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 73.3%; Score 250.8; DB 10; Length 509;
Best Local Similarity 85.4%; Pred. No. 1.1e-54;
Matches 292; Conservative 0; Mismatches 47; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACCTGCTCT 63
DB 54 GAGTGGGCCAGGACTGGTGAAGCCTTCGGAGACCCCTGTCCTCACCTGCACCTGCTCT 113

QY 64 GTGTGCTCCATCCGACGAGTGGTGGTATTATTGGAGTTGGTGGCCAGCCTCCAGGAG 123
DB 114 GGTGGCTCCATCAGCAGTAGTAGTACTCTGGGCTGGATCCGCGAGCCCCCAGGAG 173

QY 124 GGCCTGGAGTGATCGGCAACATCTATCACAGTGGCAACACCTACAAACCCGTCCTC 183
DB 174 GGCCTGGAGTGGTGGGAGTATCTATTATAGTGGGAGCACCTACTACAAACCCGTCCTC 233

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DB 234 AAGATCGAGTCACCATATCAGTAGACAGCTCCAAGAACGAGTTCTCCCTGAAGCTGAGC 293

QY 244 TCTGTGACTGCGCGACACGCGCTCTATTACTGTGGG---CGGTGAGATGGTATCTACT 300
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QY 301 TTGGACAACTGGGGCCAGGAAACCTTGTCACCGTCTCTCTCA 342
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RESULT 3

AW404242

LOCUS

AW404242 369 bp mRNA linear EST 16-FEB-2000
UI-HF-BL0-abg-f-09-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3057545 5', mRNA sequence.

ACCESSION

AW404242

VERSION

AW404242.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 369)

AUTHORS

NIH-MGC http://mgc.nci.nih.gov/.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

cDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: M13 Forward.

FEATURES

source

Location/Qualifiers

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/notes="Vector: pVT3-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

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Best Local Similarity 86.5%; Pred. No. 1.4e-54;
Matches 276; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

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Db  34  GAGTCGGCGCCAGGACTGGTAAAGCCTTCACAGACCCTGTCCTCACCTGCACTGTCTCT 93

Qy  64  GGTGGCTCCATCCCGCAGTGGTGGTTATTATTGGAGTTGGGTCCGCCAGCCTCCAGGGAAG 123
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Qy  124  GGCTTGAGTGGATCGGCAACATCTATCAGTGGCAACACTACACAAACCCGTCCTC 183
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ACCESSION  BG686767
VERSION     BG686767.1
KEYWORDS    GI:13918164
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 677)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence stop: 675.
Location/Qualifiers
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source

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/notes="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GCCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match      73.2%; Score 250.2; DB 12; Length 677;
Best Local Similarity 87.0%; Pred. No. 1.8e-54;
Matches 300; Conservative 0; Mismatches 38; Indels 7; Gaps 2;

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Qy  64  GTTGGCTCCATCCCGCAGTGGTGGTTATTATTGGAGTTGGGTCCGCCAGCCTCCAGGGAAG 123
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Db  278  AAGAGTCGAATTACCATGTCTAGTAGACGCTTAAGAACCACTTCCTCCGAGACTGACC 337

Qy  244  TCTGTGACTGCGCGGACACGGCGCTTATTACTGTGCGG-----CGTCAATGGGTAT 297
Db  338  TCTGTGACTGCGCGGACACGGCGCTTATTACTGTGCGGAGATCGCAAGAGAGAGGC 397

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5', mRNA sequence.
ACCESSION  BM783015
VERSION     BM783015.1
KEYWORDS    GI:19131247
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 607)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 2 row: E column: 06

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High quality sequence stop: 607.

FEATURES
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1..607
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S18N669761-2-E06"
/sex="F"
/lab_host="Top10F"
/clone_lib="S18N669761"
/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circualized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F, by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

ORIGIN

Query Match 73.0%; Score 249.6; DB 12; Length 607;
Best Local Similarity 84.8%; Pred. No. 2.5e-54;
Matches 295; Conservative 0; Mismatches 44; Indels 9; Gaps 1;

QY 4 GAGTGTGCGCCAGGACTGTGAAGCCTTACAGACCCCTGTCCTCACCTGCACTGCTCTCT 63
DB 112 GAGTGTGCGCCAGGACTGTGAAGCCTTACAGACCCCTGTCCTCACCTGCACTGCTCTCT 171
QY 64 GGTGGCTCCATCCGCGAGTGGTGGTTATTATTGGAGTTGGTCCGCGAGCCTCCAGGGAAG 123
DB 172 GGTGGCTCCATGAACAGTGGTAGTTACTACTGGAGTGGATCGGCAACACCCAGGGAAG 231
QY 124 GGCCTGGAGTGTGCGCAACATCTATCAGTGGCAACCTTACAGACCCGCTCCCTC 183
DB 232 GGCCTGGAGTGGTAGTTGGTGTACATCTATCAGTGGGAGCAGCTACTACAACCCGCTCCCTC 291
QY 184 AAGAGTGTGAATTTACCATGTCACTAGACAGCTTAAGAACCACTTCTCCCTGAGAGTGAAC 243
DB 292 AAGAGTGTGAATTTACCATGTCACTAGACAGCTTAAGAACCACTTCTCCCTGAGAGTGAAC 351
QY 244 TCTGTGACTGCGCGGACACGCGCTCTATTACTGTGCGCG-----GTGAGATGGG 294
DB 352 TCTGTGACTGCGCGGACACGCGCGTTTATTACTGTGCGAGAGATGGCAATTTACGATATT 411
QY 295 TATACCTTTGGCAACTGGGGCCAGGAAACCTTGTTCACCGTCTCTCTCA 342
DB 412 TACGATGTGGAGCTGTGGGGCCAGGAGCAACCGGTCAACCGTCTCTCTCA 459

RESULT 6
CD689564
LOCUS
DEFINITION
EST6087 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION
CD689564
VERSION
CD689564.1 GI:32209443
KEYWORDS
EST.
SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 490)
AUTHORS
Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and
Zeng, Y.-X.
TITLE
Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL
Unpublished (2003)

COMMENT

Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.

FEATURES
source

1..490
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

ORIGIN

Query Match 72.6%; Score 248.2; DB 14; Length 490;
Best Local Similarity 85.0%; Pred. No. 5.3e-54;
Matches 290; Conservative 0; Mismatches 48; Indels 3; Gaps 1;
QY 5 AGTCTGCGCCAGGACTGTGAAGCCTTACAGACCCCTGTCCTCACCTGCACTGCTCTG 64
DB 111 AGTCTGCGCCAGGACTGTGAAGCCTTACAGACCCCTGTCCTCACCTGCACTGCTCTG 170
QY 65 GTGGCTCCATCCGCGAGTGGTGGTTATTATTGGAGTTGGTCCGCGAGCCTCCAGGGAAG 124
DB 171 GTGGCTCCATCAGCAGTGTGGTTACTACTGGAGTTGGATTCGCCAGCACCAGGGAAG 230
QY 125 GCCTGGAGTGGATCGGCAACATCTATCAGTGGCAACACCTTACAAACACCCGTCCTCTCA 184
DB 231 GCCTGGAGTGGATTCGGGTACATCTATCAGTGGGAGTGGCGACTACACCCGTCCTCTCA 290
QY 185 AGAGTCGAATTCACATGTCACTAGACAGCTTAAGAACCACTTCTCCCTGAGAGTGAAC 244
DB 291 AGAGTCGAATTCACATGTCACTAGACAGCTTAAGAACCACTTCTCCCTGAGAGTGAAC 350
QY 245 CTGTGACTGCGCGGACACGCGCTTATTACTGTGCGCGGTTCAGAT---GGGTATAC 301
DB 351 CTGTGACGCGCGGACACGCGCTTATTACTGTGCGAGAAATGGGTCCCGAGCAGATAA 410
QY 302 TGGCAACTGGGGCCAGGGAACCTTGTGTCACCGTCTCTCTCA 342
DB 411 TTGACTACTGGGGCCAGGGAATCCTGGTCACCGTCTCTCTCA 451

RESULT 7
BG431274

LOCUS
DEFINITION
602499844F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4613435 5',
mRNA sequence.

ACCESSION
BG431274
VERSION
BG431274.1 GI:13337780
KEYWORDS
EST.
SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS

1 (bases 1 to 725)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

JOURNAL
COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
<http://image.llnl.gov>
Plate: LLCM1363 row: h column: 12

High quality sequence stop: 716.

FEATURES

source
1. .725
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4613435"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NIH_MGC_75"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcgctcgcc); Site 2: SfiI (ggcattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGCCCGGCGGCGGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

Query Match 70.6%; Score 241.4; DB 12; Length 725;
Best Local Similarity 82.0%; Pred. No. 3.7e-52;
Matches 278; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

ORIGIN

QY 4 GAGTCTGCGCCAGACTGGTGAAGCCTTCACAGACCTCTGCCCTCAGCTGACTGTCTCT 63
Db 109 GAGTGGGGCCCAAGACTGGTGAAGCCTTCGCGGACCTGTCCCTCAGCTGACTGTCTCT 168
QY 64 GGTGGCTCCATCCGACGTGGTGGTATTATTGGAGTTGGGTCCGCCAGCTCCAGGGAAG 123
Db 169 GGTGGCTCCATCATCATGTCCTCCATTATTACTGGGGCTGGATCCGCCAGCCCGCAGGGAAG 228
QY 124 GGCCTGAGTGGATCGGCAACATCTACAGTGGGCAACCTTACACAAACCCGTCCTC 183
Db 229 GGGCTGAGTGGATGTCAGTATCTCTCAGAGTGGGACCTTACTCAACCCGTCCTC 288
QY 184 AAGAGTCGATTACCATGTCAGTAGACAGCTCTAAGAACCATCTCTCCCTGAGACTGACC 243
Db 289 GAGAGTCGAGTCAACATATCGTAGACAGCTCCCAAGAACAGTTCTCCCTGAGGCTGAGG 348
QY 244 TCTGTGACTGCGGGGACAGCGCGTCTATTACTGTGCGGGTCCAGATGGGTATCTTTG 303
Db 349 CCTGTGACCGCCGAGACAGCTCTGTATATTGTGCGAGATTACTCGGGGGGAGTTT 408
QY 304 GACAATGGGGCCAGGGAACCTGGTCAACCTGTCTCTCA 342
Db 409 GACTATTGGGGCCAGGGAACCTGGTCCGCTCTCTCA 447

RESULT 8

AUI34293
LOCUS AUI34293 OVARC1 Homo sapiens cDNA clone OVARC1001672 5', mRNA
DEFINITION AUI34293 643 bp mRNA linear EST 01-AUG-2002
sequence.

ACCESSION AUI34293

VERSION AUI34293.1 GI:10994832

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 643)

AUTHORS Oca, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T.

TITLE HRI human cDNA project

JOURNAL Unpublished (2000)

CONTACT: Takao Isogai

Genomics Laboratory

Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3975

FEATURES

source
1. .643
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="OVARC1001672"
/tissue_type="ovary, tumor tissue"
/clone_lib="OVARC1"
/note="Vector: pME18SFL3"

ORIGIN

Query Match 70.5%; Score 241.2; DB 9; Length 643;
Best Local Similarity 82.9%; Pred. No. 4e-52;
Matches 295; Conservative 0; Mismatches 43; Indels 18; Gaps 1;

QY 5 AGTCTGCCCCAGACTGGTGAAGCCTTCACAGACCTCTGCCCTCAGCTGACTGTCTCTG 64
Db 110 AGTGGGCCAGACTGGTGAAGCCTTCACAGACCTCTGCCCTCAGCTGACTGTCTCTG 169
QY 65 GTGGCTCCATCCGACGTGGTGGTATTATTGGAGTTGGGTCCGCCAGCCTCCAGGGAAG 124
Db 170 GTGGCTCCATCAGCAGTGGTGGTATTCTTGGACCTGGATCCGCCAACACCCAGGGAAG 229
QY 125 GCTGGAGTGGATCGGCAACATCTACAGACCTGGCACACCTACACAAACCCGTCCTCA 184
Db 230 GCCTTGGAGTGGATGGGTATCTATTACAGTGGGACCACTACTACAAACCCGTCCTCA 289
QY 185 AGAGTCGAATTACCATGTCTAGTAGACACAGCTCTAAGAACCACTTCTCCCTGAGACTGACCT 244
Db 290 AGAGTCGAGTTACCATATCAATAGACACAGCTTAAGAACCACTTCTCCCTGAGCTGAGCG 349
QY 245 CTGTGACTGCGCGGACACGCGCGTCTATTACTGTGCGCGGTGAGATGGGTATCTACT --- 300
Db 350 CTGTGACTGCGCGGACACGCGCGTCTATTACTGTGCGAGTTTGTAGACCTTAAATAGTG 409
QY 301 -----TTGGCAACTGGGGCCAGGGAACCTGGTCCAGCTGCTCTCA 342
Db 410 GGACCTACAGTAAGTTTGACCACTGGGGCCAGGGAACCTGGTCCAGCTGCTCTCA 465

RESULT 9

BQ710488

LOCUS BQ710488

DEFINITION BQ710488 904 bp mRNA linear EST 16-JUL-2002

5', mRNA sequence.

ACCESSION BQ710488

VERSION BQ710488.1 GI:21849387

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 904)

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE NIH-MGC http://mgi.nci.nih.gov/

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov

Tissue Procurement: Dr. Mark Watson

cDNA Library Preparation: Rubin Laboratory

DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov

Plate: L1CM2465 row: k column: 02

High quality sequence stop: 728.

Fax: 81-438-52-3986

Email: genomics@hri.co.jp

HRI human cDNA project; 5' and 3'-end one pass sequencing: Helix

Research Institute; cDNA library construction: Department of

Virology, Institute of Medical Science, University of Tokyo, and

Helix Research Institute.

FEATURES
source

Location/Qualifiers
1. .904
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6278137"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 70.2%; Score 240; DB 13; Length 904;
Best Local Similarity 83.0%; Pred. No. 9.6e-52;
Matches 289; Conservative 0; Mismatches 50; Indels 9; Gaps 1;

QY 4 GAGTCTGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACCTGCTCTCT 63
DB 86 GAGTCGGGCCAGGACTGGTGAAGCCTTCGGAGACCCCTGTCCTCACCTGCACCTGCTCTCT 145

QY 64 GGTGGCTCCATCCGAGTGGTGTATTATTGGAGTTGGTCCGCGAGCCTCCAGGGAAG 123
DB 146 GGTGGCTCCATCAGCAGTAGTACTGCTGGGCTGGATCCGCGAGCCTCCAGGGAAG 205

QY 124 GGCCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTACAAACCCGTCCTC 183
DB 206 GGCCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTACAAACCCGTCCTC 265

QY 184 AAGAGTCGAATTACATGTCTAGTAGACACGCTTAAGAACCTCTTCCCTGAGACTGACC 243
DB 266 AAGAGTCGAGTCACCATATCCGTAGACACGCTCCAGAACCTCTTCCCTGAGACTGACC 325

QY 244 TCTGTGACTGCGCGGACACGCGCTCTATTACTGTGCGGCTCAGA-----TGGG 294
DB 326 TCTGTGACTGCGCGGACACGCGCTCTATTACTGTGCGGCTCAGA-----TGGG 385

QY 295 TATACCTTTGGACAACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342
DB 386 CATTACTTCCAGCACTGGGGCCAGGCAACCCCTGGTCAACCGTCTCTCTCA 433

RESULT 10
BU899307

LOCUS BU899307 959 bp mRNA linear EST 17-OCT-2002
DEFINITION AGENCOURT 8532130 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6280128 5', mRNA sequence.

ACCESSION BU899307
VERSION BU899307.1 GI:24081220
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 959)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLCM2470 row: n column: 01

FEATURES
source

High quality sequence stop: 605.
Location/Qualifiers
1. .959
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6280128"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 70.1%; Score 239.8; DB 13; Length 959;
Best Local Similarity 83.2%; Pred. No. 1.1e-51;
Matches 287; Conservative 0; Mismatches 52; Indels 6; Gaps 1;

QY 4 GAGTCTGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACCTGCTCTCT 63
DB 86 GAGTCGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACCTGCTCTCT 145

QY 64 GGTGGCTCCATCCGAGTGGTGTATTATTGGAGTTGGTCCGCGAGCCTCCAGGGAAG 123
DB 146 GGTGGCTCCATCAGCAGTAGTATTCTTCTGGAGTGGATCCGCGAGTCTCCAGGGAAG 205

QY 124 GGCCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTACAAACCCGTCCTC 183
DB 206 GGCCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTACAAACCCGTCCTC 265

QY 184 AAGAGTCGAATTACATGTCTAGTAGACACGCTTAAGAACCTCTTCCCTGAGACTGACC 243
DB 266 AGGCGTCGAGTTACCATATCATACAGACGCTCCAGAACCTCTTCCCTGAGACTGACC 325

QY 244 TCTGTGACTGCGCGGACACGCGCTCTATTACTGTGCGGCTCAG-----ATGGGTAT 297
DB 326 TCTGTGACTGCGCGGACACGCGCTCTATTACTGTGCGGCTCAG-----ATGGGTAT 385

QY 298 ACTTTGGACAACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342
DB 386 GCTTTTGATATCTGGGGCCAGGGAACCTGGTCAACCGTCTCTCTCA 430

RESULT 11
BX324929

LOCUS BX324929 890 bp mRNA linear EST 02-MAY-2003
DEFINITION BX324929 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSOD1086YU13 5-PRIME, mRNA sequence.

ACCESSION BX324929
VERSION BX324929.1 GI:30338413
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 890)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seq@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7198.r For more information about this cluster, see <http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSOA1086CE070P1&cluster=7198.r>. Contact :

Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> InvitroGen Corporation 1600
 Faraday Avenue Genescope sequence ID : CS0AI086CE07QPI.
 Location/Qualifiers
 1. .890
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DI086J13"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dfr)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and BclI V
 sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES

source

ORIGIN

Query Match 69.8%; Score 238.8; DB 13; Length 890;
 Best Local Similarity 82.5%; Pred. No. 2e-51;
 Matches 292; Conservative 0; Mismatches 47; Indels 15; Gaps 1;
 QY 4 GAGTCTGCCCGCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCAGCTGCACTGTCTCT 63
 Db |||||
 133 GAGTCGGGCCCGAGGACTGGTGAAGCCTTCGGAGACCCCTGTCCTCAGCTGCACTGTCTCT 192
 QY 64 GGTGGCTCCATCCGACGTGGTGGTATTATTGGAGTTGGTCCGCCAGCCCTCCAGGGAAG 123
 Db |||||
 193 GGTGGCTCCATCCGACGTGGTGGTATTATTGGAGTTGGTCCGCCAGCCCTCCAGGGAAG 252
 QY 124 GGCCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTACAAACACCCGTCCCTC 183
 Db |||||
 253 GGGCTGAGTGGATGGGACTATCTATTATAGTGGAGACACTACTACACCCGTCCCTC 312
 QY 184 AAGAGTCCGATTACCATGTCTAGTAGACACGCTTAAAGAACCACTTCTCCCTGAGACTGACC 243
 Db |||||
 313 AAGAGTCCGATCCATATAGTAGACACGCTTAAAGAACCACTTCTCCCTGAGCTGAGC 372
 QY 244 TCTGTGACTCGCGGACACGGCGCTTATTACTGTGGCGGTGAGTGGTAT----- 297
 Db |||||
 373 TCTGTGACCGCGCGGACACGGCGGTGATTACTGTGCGAGTGGTGTAGTGGTATGAGC 432
 QY 298 -----ACTTTGGACAACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA 342
 Db |||||
 433 TGCTACCTCGCTTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA 486

RESULT 12

BQ706579

LOCUS

DEFINITION AGENCOURT_8487944 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6300935
 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov

Tissue Procurement: Dr. Mark Watson

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LCM2515 row: p column: 24

High quality sequence start: 4

FEATURES

source

High quality sequence stop: 584.
 Location/Qualifiers
 1. .903
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGB:6300935"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_113"
 /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACAGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN

Query Match 69.6%; Score 238.2; DB 13; Length 903;
 Best Local Similarity 82.9%; Pred. No. 2.8e-51;
 Matches 286; Conservative 0; Mismatches 53; Indels 6; Gaps 1;
 QY 4 GAGTCTGCCCGCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCAGCTGCACTGTCTCT 63
 Db |||||
 98 GAGTCGGGCCCGAGGACTGGTGAAGCCTTCGGAGACCCCTGTCCTCAGCTGCACTGTCTCT 157
 QY 64 GGTGGCTCCATCCGACGTGGTGGTATTATTGGAGTTGGTCCGCCAGCCCTCCAGGGAAG 123
 Db |||||
 158 GGTGGCTCCATCCGACGTGGTGGTATTATTGGAGTTGGTCCGCCAGCCCTCCAGGGAAG 217
 QY 124 GGCCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTACAAACACCCGTCCCTC 183
 Db |||||
 218 GGGCTGAGTGGATGGGAAATATCGATTATAGTGGAGCATCTACTACAAACCCGTCCCTC 277
 QY 184 AAGAGTCCGATTACCATGTCTAGTAGACACGCTTAAAGAACCACTTCTCCCTGAGACTGACC 243
 Db |||||
 278 AAGAGTCCGATCCATATCGTAGACACGCTTAAAGAACCACTTCTCCCTGAGACTGAGG 337
 QY 244 TCTGTGACTCGCGGACACGGCGCTCTATTACTGTGC-----CGCGTCAGATGGGTAT 297
 Db |||||
 338 TCTGTGACCGCGGACACGGCGCTCTATTACTGTGGAAAGGGGCATAGTTATGGGC 397
 QY 298 ACTTTGAGAACCTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA 342
 Db |||||
 398 TGGTTCGACCCCTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA 442

RESULT 13

BQ920469

LOCUS

DEFINITION AGENCOURT_6709612 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5750444
 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLM12781 row: g column: 21

High quality sequence stop: 626.

FEATURES

source

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1. 1108
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="IMAGE:575044"
/lab_host="DH10B"
/clone_lib="NIH_MGC_122"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."

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ORIGIN

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Query Match      69.6%; Score 238.2; DB 12; Length 1108;
Best Local Similarity 82.9%; Pred. No. 3.1e-51;
Matches 286; Conservative 0; Mismatches 53; Indels 6; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCCTCAGCTGCACTGTCTCT 63
Db 110 GAGTCGGGCCAGGACTGGTGAAGCCTTCGGAGACCTGTCCTCCTCAGCTGCACTGTCTCT 169
QY 64 GGTGGCTCATCCGAGTGGTGGTTATTATTGGAGTTGGGTCCGCGAGCTCCAGGGAAG 123
Db 170 GGTGGCTCCGTGAGCAGTGGTGGTTACTACTGGAGCTGGATCCGCGAGCCCCCAGGGAAG 229
QY 124 GGCCTGGAGTGGATCGGCAACATCTATCAGTGGCAGACCTTACACAAACCCGTCCTC 183
Db 230 GGACTGGAGTGGATGGGTATATCTATTACAGTGGGAGCACCACCTACAAACCCCTCCCTC 289
QY 184 AAGAGTCGAATTACCATGTCTAGTAGACACGCTCTAAGAACCACTTCTCCCTGAGACTGACC 243
Db 290 AAGAGTCGAGTCACCATATCAGTAGACACGCTCAAGAACCACTTCTCCCTGAGCTGACC 349
QY 244 TCTGTGACTGCGCGGACACGCGCGTCTATTACTGTGGCGGTCTGATGGG-----TAT 297
Db 350 TCTGTGACCGTGGCGACACGCGCGTGTATTACTGTGGAGCGGGGGGGGGGAGACTAC 409
QY 298 ACTTTGGACAACTGGGGCCAGGGAACCCCTGGTCACCGTCTCTCTCA 342
Db 410 TACATGGACGCTGGGGGCAAGGACCAACGCGTCAACCGTCTCTCTCA 454

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RESULT 14

BX336901

LOCUS

DEFINITION BX336901 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0D1034Y102 5-PRIME, mRNA sequence.

ACCESSION

BX336901

VERSION

BX336901.1

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 977)

AUTHORS

Li, W.B., Gruber, C., Jessee, J., and Polayes, D.

TITLE

Full-length cDNA libraries and normalization

JOURNAL

Unpublished (2001)

COMMENT

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 7198.r For

more information about this cluster, see

<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0D1026BC04Op1&cluster=7198.r>. Contact :

Feng Liang Email: fliang@lifetech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0D1026BC04QPl.

Location/Qualifiers

1. 977

/organism="Homo sapiens"

/mol_type="mrna"

/db_xref="taxon:9606"

/clone="CS0D1026YE08"

/tissue type="PLACENTA COT 25-NORMALIZED"

/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

Query Match 69.4%; Score 237.2; DB 13; Length 977;

Best Local Similarity 82.2%; Pred. No. 5.3e-51;

Matches 291; Conservative 0; Mismatches 48; Indels 15; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCCTCAGCTGCACTGTCTCT 63

Db 163 GAGTCGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCCTCAGCTGCACTGTCTCT 222

QY 64 GGTGGCTCATCCGAGTGGTGGTTATTATTGGAGTTGGGTCCGCGAGCTCCAGGGAAG 123

Db 223 GGTGGCTCCATCAGCAGTGGTAGTTACTACTGGAGCTGGATCCGCGAGCCCCCAGGGAAG 282

QY 124 GGCCTGGAGTGGATCGGCAACATCTATCAGTGGCAGACCTTACAAACCCGTCCTC 183

Db 283 GGACTGGAGTGGATGGGCGGTATCTATACAGTGGGAGCACCACCTACAAACCCCTCCCTC 342

QY 184 AAGAGTCGAATTACCATGTCTAGTAGACACGCTCTAAGAACCACTTCTCCCTGAGACTGACC 243

Db 343 AAGAGTCGAGTCACCATATCAGTAGACACGCTCAAGAACCACTTCTCCCTGAAAGCTGAGC 402

QY 244 TCTGTGACTGCGCGGACACGCGCGTCTATTACTGTGGG-----CGGTCA 288

Db 403 TCTGTGACCGCGCGAGACACGCGCGTGTATTACTGTGCGATCACCAGATAGTGCGTAC 462

QY 289 GATGGGTATACTTTGGACAACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342

Db 463 GATGAGGCGCTGTTTGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 516

RESULT 15

BX336959

LOCUS

DEFINITION BX336959 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0D1034Y102 5-PRIME, mRNA sequence.

ACCESSION

BX336959

VERSION

BX336959.1

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 1201)

AUTHORS

Li, W.B., Gruber, C., Jessee, J., and Polayes, D.

TITLE

Full-length cDNA libraries and normalization

JOURNAL

Unpublished (2001)

COMMENT

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 7198.r For

cgi-bin/cluster.cgi?seq=CS0DI034BE01QPI&cluster=7198.r. Contact :
Feng Liang Email : fliang@lifetech.com URL : Corporation 1600
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue denoscope sequence ID : CS0DI034BE01QPI.
Location/Qualifiers

FEATURES

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1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI034YI02"
/tissue_type="PLACENTA COT 25-NORMALIZED"
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/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 69.4%; Score 237.2; DB 13; Length 1201;
Best Local Similarity 82.2%; Pred. No. 5.8e-51;
Matches 291; Conservative 0; Mismatches 48; Indels 15; Gaps 1;
Qy 4 GAGTCTGGCCAGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACTGACTGTCTCT 63
Db |||||
156 GAGTCGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACTGACTGTCTCT 215
Qy 64 GGTGCTCCATCCCGAGTGGTGTATTATTGGAGTTGGGTCCGCGACCTCCAGGGAAG 123
Db |||||
216 GGTGCTCCATCCCGAGTGGTGTATTATTGGAGTTGGGTCCGCGACCTCCAGGGAAG 275
Qy 124 GGCCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACTACAAACCCCTCCCTC 183
Db |||||
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Qy 184 AAGAGTCGAATTACATGTCCAGTAGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 243
Db |||||
336 AAGAGTCGAGTCACCATATCAGTAGACACGCTCCAGAACCACTTCTCCCTGAAGCTGAGC 395
Qy 244 TCTGTGACTCGCGGACACGCGCTCTATTACTGTGGG-----CGGTCA 288
Db |||||
396 TCTGTGACCGCGGACACGCGCTGTATTACTGTGCGATCACCCAGCATAGTGGCTAC 455
Qy 289 GATGGGTATACCTTTGGACAACCTGGGCGCAGGGAACCTGGTCCAGCGTCTCCTCA 342
Db |||||
456 GATGAGGGCTTGTGTGACTACTGGGGCCAGGGAACCTGGTCCAGCGTCTCCTCA 509

Search completed: August 13, 2004, 07:13:19
Job time : 2007.71 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 12, 2004, 11:40:47 ; Search time 222.818 Seconds
(without alignments)
6520.490 Million cell updates/sec

Title: US-10-027-725A-2

Perfect score: 342

Sequence: 1 ctgagctgtgcccaggact.....ccctggctaccgtctctctca 342

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq 29Jan04.*

1: Geneseqn1980s.*

2: Geneseqn1980s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002s.*

7: Geneseqn2003as.*

8: Geneseqn2003bs.*

9: Geneseqn2003cs.*

10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	340.4	99.5	342	6	ABK89638 DNA encod
2	324.4	94.9	342	6	ABK89639 DNA encod
3	297.2	86.9	342	6	ABK89637 DNA encod
4	271.8	79.5	352	9	ADC99786 Anti-huma
5	271.8	79.5	352	9	Add05390 Anti-MUC1
6	268.4	78.5	360	4	Aaf29076 Human HIV
7	262.2	76.7	352	9	Aaf29078 Anti-huma
8	262.2	76.7	352	9	Add05382 Anti-MUC1
9	260.4	76.1	358	9	ADC99798 Anti-huma
10	260.4	76.1	358	9	Add05402 Anti-MUC1
11	257.8	75.4	369	4	Aaf29046 Human HIV
12	254.8	74.5	352	9	ADC99806 Anti-huma
13	251.2	73.5	366	4	Add05410 Anti-MUC1
14	251.2	73.5	366	4	Aaf29066 Human HIV
15	251.2	73.5	516	3	Aaa46876 DNA encod
16	250.2	73.2	741	3	Aaz28998 Anti-muri
17	249.2	72.9	357	7	Aa38670 MAB GAH V
18	247.8	72.5	467	7	Ab259692 Anti-TRAI
19	244.8	71.6	504	3	Aaz42341 Human 5'
20	244.6	71.5	467	7	Ab259694 Anti-TRAI
21	244.2	71.4	381	6	Abk24408 Heavy cha
22	244.2	71.4	1644	2	Aaz24434 Human bla
23	244	71.3	378	3	Aac62336 DNA encod

24	243	71.1	340	6	ABK84446	Human cDN
25	243	71.1	340	7	ACA64884	Human Ig
26	243	71.1	450	2	AAx90024	Human mon
27	242.6	70.9	324	4	ABS46332	Human liv
28	242.6	70.9	631	2	AAQ78969	Human imm
29	240.6	70.4	360	5	Aaf29506	Human Fab
30	239.4	70.0	384	6	ABK24410	Heavy cha
31	239.2	69.9	393	3	AAC98188	Human col
32	237.8	69.5	381	6	ABK24406	Heavy cha
33	237.8	69.5	466	3	AAZ42292	Human 5'
34	237.4	69.4	1567	4	AAC66522	Human imm
35	236.8	69.2	614	2	AAV86218	EST clone
36	236.6	69.2	351	3	Az49608	DNA-1 rel
37	236.6	69.2	351	3	Az49590	Human ant
38	235	68.7	351	7	AAL50841	Human ant
39	234.6	68.6	1543	4	AAF97947	Human sec
40	234	68.4	372	4	AAF29051	Human HIV
41	231.2	67.6	417	3	Az39316	Nucleotid
42	231	67.5	360	8	ADA89197	Human ant
43	230.4	67.4	462	7	ABT31873	Anti-CD40
44	229.8	67.2	357	4	AAS03405	DNA encod
45	227.4	66.5	366	2	AAQ33035	MAB 1-3-1

ALIGNMENTS

RESULT 1

ABK89638

ID ABK89638 standard; DNA; 342 BP.

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AC ABK89638;

XX

DT 21-OCT-2002 (first entry)

XX

DE DNA encoding human IgE Fab clone 60 heavy chain.

XX

KW Human; fab; ds; gene; anti-allergic; vaccine; grass pollen; Phi p 2;

KW timothy grass pollen allergen; passive immunotherapy.

XX

OS Homo sapiens.

XX

EH Key Location/Qualifiers

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FT FT misc_feature 7..78

FT /tag= b /note= "FR1 region"

FT FT misc_feature 79..99

FT /tag= c /note= "CDR1 region"

FT FT misc_feature 100..123

FT /tag= d /note= "FR2 region"

FT FT misc_feature 134..141

FT /tag= e /note= "FR3 region"

FT FT misc_feature 142..189

FT /tag= f /note= "CDR2 region"

FT FT misc_feature 190..285

FT /tag= g /note= "FR3 region"

FT FT misc_feature 286..309

FT /tag= h /note= "CDR3 region"

FT FT misc_feature 310..342

FT /tag= i /note= "FR4 region"

XX

PN WO200253595-A1.

XX

PD 11-JUL-2002.
XX 27-DEC-2001; 2001WO-SE002908.
XX 29-DEC-2000; 2000SE-00004892.
XX (PHAA) PHARMACIA DIAGNOSTICS AB.
XX Flicker S, Steinberger P, Kraft D, Valenta R;
XX WPI; 2002-583604/62.
XX P-PSDB; ABG30446.
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX
PS Disclosure; Page 32; 45pp; English.
XX This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have antiallergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The fabs
CC - or a vaccine against a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for blocking the binding of group 2 allergen-containing pollen and
CC IgE antibodies to Phi p 2. The present sequence represents the DNA
CC encoding the human IgG fab, clone 60 heavy chain protein of the invention
XX
SQ Sequence 342 BP; 70 A; 105 C; 90 G; 77 T; 0 U; 0 Other;
Query Match 99.5%; Score 340.4; DB 6; Length 342;
Best Local Similarity 99.7%; Pred. No. 3,7e-87;
Matches 341; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CTCGAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCTGTCCCTCACTGCAGTGC 60
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1 CTCGAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCTGTCCCTCACTGCAGTGC 60
QY 61 TCTGTGGCTCCATCCGAGTGGTGGTTATTATTGGAGTTGGTCCGCCAGCTCCAGGG 120
Db |||||||
61 TCTGTGGCTCCATCCGAGTGGTGGTTATTATTGGAGTTGGTCCGCCAGCTCCAGGG 120
QY 121 AAGGCGCTGGAGTGGTGGCAACATCTATCAGTGGCAACACCTACAAACCCGTC 180
Db |||||||
121 AAGGCGCTGGAGTGGTGGCAACATCTATCAGTGGCAACACCTACAAACCCGTC 180
QY 181 CTCAGAGTCTGAATTCATGTAGTACAGCTCTAAGAACCACTTCCCTGAGACTG 240
Db |||||||
181 CTCAGAGTCTGAATTCATGTAGTACAGCTCTAAGAACCACTTCCCTGAGACTG 240
QY 241 ACCTCTGTACTGCGCGGACACCGCGTCTATTACTGTGGCGTTCAGATGGGTACT 300
Db |||||||
241 ACCTCTGTACTGCGCGGACACCGCGTCTATTACTGTGGCGTTCAGATGGGTACT 300
QY 301 TTGACAACTGGGGCCAGGAAACCTTGGTTCACCGTCTCTCTCA 342
Db |||||||
301 TTGACAACTGGGGCCAGGAAACCTTGGTTCACCGTCTCTCTCA 342
RESULT 2
ID ABR89639
XX ABR89639 standard; DNA; 342 BP.
AC ABR89639;
XX

DT 21-OCT-2002 (first entry)
XX DNA encoding human IgE Fab clone 100 heavy chain.
XX Human; fab; ds; gene; antiallergic; vaccine; grass pollen; Phi p 2;
KW timothy grass pollen allergen; passive immunotherapy.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 1..342
FT /tag= a
FT /product= "Fab clone 100 heavy chain"
FT misc_feature 7..78
FT /tag= b
FT /note= "FR1 region"
FT misc_feature 79..99
FT /tag= c
FT /note= "CDR1 region"
FT misc_feature 100..123
FT /tag= d
FT /note= "FR2 region"
FT misc_feature 134..141
FT /tag= e
FT /note= "FR3 region"
FT misc_feature 142..189
FT /tag= f
FT /note= "CDR2 region"
FT misc_feature 190..285
FT /tag= g
FT /note= "FR3 region"
FT misc_feature 286..309
FT /tag= h
FT /note= "CDR3 region"
FT misc_feature 310..342
FT /tag= i
FT /note= "FR4 region"
XX
XX WO200253595-A1.
XX 11-JUL-2002.
XX 27-DEC-2001; 2001WO-SE002908.
XX 29-DEC-2000; 2000SE-00004892.
XX (PHAA) PHARMACIA DIAGNOSTICS AB.
XX Flicker S, Steinberger P, Kraft D, Valenta R;
XX WPI; 2002-583604/62.
XX P-PSDB; ABG30447.
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX
PS Disclosure; Page 33; 45pp; English.
XX This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have antiallergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The fabs
CC - or a vaccine against a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergic patients

CC IGE antibodies to Phi p 2. The present sequence represents the DNA
 CC encoding the human Igg fab, clone 100 heavy chain protein of the
 CC invention
 XX
 XX
 SQ Sequence 342 BP; 69 A; 103 C; 94 G; 76 T; 0 U; 0 Other;
 Query Match 94.9%; Score 324.4; DB 6; Length 342;
 Best Local Similarity 96.8%; Pred. No. 1.4e-82;
 Matches 331; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 QY 1 CTCGAGTCTGGCCAGGACTGGTGAAGCCTTTCACAGACCCCTGTCCCTCACCTGCACCTGTC 60
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 DB 1 CTCGAGTCTGGCCAGGACTGGTGAAGCCTTTCACAGACCCCTGTCCCTCACCTGCACCTGTC 60
 QY 61 TCTGGTGGCTCCATCCGAGTGGTGGTATTTATTTGGAGTTGGGTCCGCGACCTCCAGGG 120
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 DB 61 TCTGGTGGCTCCATCCGAGTGGTGGTATTTATTTGGAGTTGGGTCCGCGACCTCCAGGG 120
 QY 121 AAGGCGCTGGAGTGGATCGGCAACATCTATCACAGTGGCACACTACACACCCGTC 180
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 DB 121 AAGGCGCTGGAGTGGATCGGGTACATCTATCACAGTGGCACACTACACTACACCCGTC 180
 QY 181 CTCGAAGAGTCCGAATTACCATGTCTAGTAGACACAGCTTAAGAACCACTTCTCCCTGAGACTG 240
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 DB 181 CTCGAAGAGTCCGATTACCATGTCTAGTAGACACAGCTTAAGAACCACTTCTCCCTGAGGCTG 240
 QY 241 ACCTCTGTGACTGCCGGACACGCGGTCTATTACTGTGGCGGTGAGATGGGTACTACT 300
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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 QY 301 TTGGACAACCTGGGCGGAGGAAACCCCTGGTCAACCGTCTCTCTCA 342
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 DB 301 TTGGACAACCTGGGCGGAGGAAACCCCTGGTCAACCGTCTCTCTCA 342

RESULT 3
 ABK89637
 ID ABK89637 standard; DNA; 342 BP.
 AC ABK89637;
 DT 21-OCT-2002 (first entry)
 XX DNA encoding human Ige Fab clone 94 heavy chain.
 XX Human; fab; ds; gene; antiallergic; vaccine; grass pollen; Phi p 2;
 KW timothy grass pollen allergen; passive immunotherapy.
 XX Homo sapiens.
 FH Key Location/Qualifiers
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 FT misc_feature 7..78
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FT /*tag= h
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 FT /note= "FR4 region"
 XX WO200253595-A1.
 XX 11-JUL-2002.
 XX 27-DEC-2001; 2001WO-SB002908.
 XX 29-DEC-2000; 2000SE-00004892.
 XX (PHAA) PHARMACIA DIAGNOSTICS AB.
 XX Flicker S, Steinberger P, Kraft D, Valenta R;
 XX WPI; 2002-583604/62.
 XX P-FSD; ABG30445.
 XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
 XX variable region of group 2 allergen specific-human Ige Fabs, useful for
 XX diagnosing or passive immunotherapy of type I allergy, for environmental
 XX allergen detection.
 XX Disclosure; Page 31-32; 45pp; English.
 XX This invention relates to the DNA and protein sequences of group 2
 XX allergen-specific human Ige Fabs and methods for their use. The proteins
 XX of the invention may have antiallergic activities and may be used as a
 XX vaccine or an inhibitor of binding of grass pollen allergen patient's Ige
 XX antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
 XX 2 allergen-specific fabs of the invention may be useful for environmental
 XX allergen detection and for standardisation of allergen extracts. The fabs
 XX - or a vaccine against a type I allergy is useful for passive
 XX immunotherapy of type I allergy, it is also useful for diagnosing a type
 XX I allergy. The allergen-specific fabs of the invention are useful for
 XX inter alia, diagnosis, therapy and prevention of type I allergy. They are
 XX also useful for identification of group 2 allergen-containing pollen and
 XX may be used for blocking the binding of grass pollen allergic patients
 XX Ige antibodies to Phi p 2. The present sequence represents the DNA
 XX encoding the human Ige fab, clone 94 heavy chain protein of the invention
 XX
 SQ Sequence 342 BP; 69 A; 100 C; 98 G; 75 T; 0 U; 0 Other;
 Query Match 86.9%; Score 297.2; DB 6; Length 342;
 Best Local Similarity 91.8%; Pred. No. 7.8e-75;
 Matches 314; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
 QY 1 CTCGAGTCTGGCCAGGACTGGTGAAGCCTTTCACAGACCCCTGTCCCTCACCTGCACCTGTC 60
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 DB 1 CTCGAGTCTGGCCAGGACTGGTGAAGCCTTTCACAGACCCCTGTCCCTCACCTGCACCTGTC 60
 QY 61 TCTGGTGGCTCCATCCGAGTGGTGGTATTTATTTGGAGTTGGGTCCGCGACCTCCAGGG 120
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 DB 61 TCTGGTGGCTCCATCCGAGTGGTGGTATTTATTTGGAGTTGGGTCCGCGACCTCCAGGG 120
 QY 121 AAGGCGCTGGAGTGGATCGGCAACATCTATCACAGTGGCACACTACACTACACCCGTC 180
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 DB 121 AAGGCGCTGGAGTGGATTTGGGTACATCTATCACAGTGGAACACTACTACTACACCCGTC 180
 QY 181 CTCGAAGAGTCCGAATTACCATGTCTAGTAGACACAGCTTAAGAACCACTTCTCCCTGAGACTG 240
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 DB 181 CTCGAAGAGTCCGAATTGCGGTATGCGTAGACACGCTCTGAGAACAAGTTCTCCCTGAGGCTG 240
 QY 241 ACCTCTGTGACTGCCGGACACGCGGTCTATTACTGTGGCGGTGAGATGGGTACTACT 300
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 DB 241 AACTCTGTGACTGCCGGACACGCGGTGATTACTGTGGAGGTAGATGGGTACTACT 300
 QY 301 TTGGACAACCTGGGCGGAGGAAACCCCTGGTCAACCGTCTCTCTCA 342
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 DB 301 TTGGACAACCTGGGCGGAGGAAACCCCTGGTCAACCGTCTCTCTCA 342

```
RESULT 4
ID ADC99786
XX ADC99786 standard; DNA; 352 BP.
AC ADC99786;
DT 01-JAN-2004 (first entry)
DE Anti-human MUC18 antibody heavy chain variable domain DNA SEQ ID 15.
XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
KW lung cancer; human; ds; gene.
XX Homo sapiens.
OS
XX WO2003057838-A2.
PN 17-JUL-2003.
XX 26-DEC-2002; 2002WO-US041581.
PF 28-DEC-2001; 2001US-0346299P.
XX (ABGE-) ABGENIX INC.
PA Gudas J;
PI
XX WPI; 2003-587113/55.
DR P-PSDB; ADC99784.
XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease
PT or condition associated with expression of MUC18 in a patient, e.g.
PT tumors, cancers, and other malignancies.
XX Claim 8; SEQ ID NO 15; 78pp; English.
XX The invention relates to a novel isolated monoclonal antibody comprising
CC a heavy or light chain amino acid or a heavy or light chain variable
CC domain where the antibody binds to MUC18. The monoclonal antibody of the
CC invention demonstrates cytostatic activity and may be useful for treating
CC a disease or condition associated with the expression of MUC18 on the
CC cell surface such as tumours, specifically melanoma, oesophageal,
CC pancreatic or colorectal tumours, carcinomas, particularly cervical
CC carcinomas and cervical intraepithelial neoplasia and cancers including
CC colorectal, breast or lung cancer, as well as other malignancies. The
CC current sequence is that of the anti-human MUC18 monoclonal antibody
CC heavy chain variable domain DNA of the invention.
XX Sequence 352 BP; 73 A; 100 C; 103 G; 76 T; 0 U; 0 Other;
SQ
Query Match 79.5%; Score 271.8; DB 9; Length 352;
Best Local Similarity 89.7%; Pred. No. 1.4e-67;
Matches 304; Conservative 0; Mismatches 32; Indels 3; Gaps 1;
QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCAGCTGTCCT 63
DB 16 GAGTGGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCAGCTGTCCT 75
QY 64 GGTGGCTCCATCCGAGTGGTGGTTATTATTGGAGTTGGGTCCGCGACCCCTCCAGGGGAG 123
DB 76 GGTGGCTCCATCCGAGTGGTGGTTATTATTGGAGTTGGGTCCGCGACCCCTCCAGGGGAG 135
QY 124 GGCTGGAGTGGATCGGCAACATCTATCAGAGTGGCAACCTACAAACCGTCCCTC 183
DB 136 GGCTGGAGTGGATGGGTTTCATCTATTACAGTGGAGCACTACTACAAACCGTCCCTC 195
QY 184 AAGAGTCCGAATTACATGTCAGTAGACACGCTCTAAGAACCACTTCTCCCTGAGACTGACC 243
DB 196 AAGAGTCCGATTACCATATCAGTAGACACGCTCTAAGAACCACTTCTCCCTGAGCTGAGC 255
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QY 244 TCTGTGACTGCGCGGACACGGCGCTCTATTACTGTGCGCGTCCAGATGGGTATCTTTG 303
DB 256 TCTGTGACTGCGCGGACACGGCGCTCTATTACTGTGCGGAG--AGAGGAGATGGCTTT 312
QY 304 GACAACTGGGGCCAGGGAACCTGTGTACCGTCTCTCTCA 342
DB 313 GACTACTGGGGCCAGGGAACCTGTGTACCGTCTCTCTCA 351
RESULT 5
ID ADD05390
XX ADD05390 standard; DNA; 352 BP.
AC ADD05390;
XX 01-JAN-2004 (first entry)
DT Anti-MUC18 antibody heavy chain variable region DNA, SEQ ID NO 15.
DE Anti-MUC18 antibody heavy chain variable region DNA, SEQ ID NO 15.
XX monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain;
KW gene; ds.
XX Homo sapiens.
OS
XX WO2003057006-A2.
PN 17-JUL-2003.
XX 26-DEC-2002; 2002WO-US041582.
PF 28-DEC-2001; 2001US-0346460P.
XX (ABGE-) ABGENIX INC.
PA Gudas J, Bar-Eli M;
PI
XX WPI; 2003-577496/54.
DR P-PSDB; ADD05388.
XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT associated with melanoma, or increasing survival of an animal having a
PT metastatic tumor.
XX Disclosure; SEQ ID NO 15; 87pp; English.
XX The invention relates to a novel monoclonal antibody used for inhibiting
CC tumour growth in an animal. The tumour inhibition process comprises
CC selecting an animal in need of treatment for a tumour, providing a
CC monoclonal antibody comprising a heavy chain amino acid, where the
CC antibody consists of any one of 10 fully defined sequences of 117-123
CC amino acids given in the specification, and where the monoclonal antibody
CC binds MUC18, and contacting the tumour with the antibody resulting in
CC inhibited proliferation of the cells. The monoclonal antibody has
CC cytostatic and can be used in the production of a vaccine. The monoclonal
CC antibodies against the MUC18 antigen are useful for diagnosing and
CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
CC increasing survival of an animal having a metastatic tumour. This
CC polynucleotide sequence represents the DNA encoding an anti-MUC18
CC antibody heavy chain, variable region, protein of the invention.
XX Sequence 352 BP; 73 A; 100 C; 103 G; 76 T; 0 U; 0 Other;
SQ
Query Match 79.5%; Score 271.8; DB 9; Length 352;
Best Local Similarity 89.7%; Pred. No. 1.4e-67;
Matches 304; Conservative 0; Mismatches 32; Indels 3; Gaps 1;
QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCAGCTGTCCT 63
DB 16 GAGTGGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCAGCTGTCCT 75
```

QY 64 GGTGGCTCCATCCGACGTGGTGTATTATTATTTGGAGTTGGGTCCGCCAGCCTCCAGGGAAG 123
 Db 76 GGTGGCTCCATCCGACGTGGTGTATTATTATTTGGAGTTGGGTCCGCCAGCCTCCAGGGAAG 135
 QY 124 GGCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTACAAACCCGTCCTC 183
 Db 136 GGCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTACAAACCCGTCCTC 195
 QY 184 AAGAGTCGAATTACCATGTTCAGTAGACACGCTCTAAGAACCATTTCTCCCTGAGACTGACC 243
 Db 196 AAGAGTCGAGTTACCATATCAGTAGACACGCTCTAAGAACCATTTCTCCCTGAGACTGAGC 255
 QY 244 TCTGTGACTCGCGGACACGGCCGCTATTACTGTGGCGGTGAGATGGGTACTATTG 303
 Db 256 TCTGTGACTCGCGGACACGGCCGCTATTACTGTGGCGGTGAGATGGGTACTATTG 312
 QY 304 GACAACTGGGGCCAGGGAACCCCTGGTCACCGCTCTCCTCA 342
 Db 313 GACTACTGGGGCCAGGGAACCCCTGGTCACCGCTCTCCTCA 351

RESULT 6

AAF29076
 ID AAF29076 standard; DNA; 360 BP.

AC AAF29076;

XX 03-APR-2001 (first entry)

XX Human HIV-1 monoclonal antibody coding sequence SEQ ID NO: 32.

XX Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
 KW envelope glycoprotein; gp120; diagnosis; ds.

XX Homo sapiens.

XX WO200100678-A1.

XX 04-JAN-2001.

XX 23-JUN-2000; 2000WO-US017327.

XX 30-JUN-1999; 99US-0141701P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Watkins BA, Reitz MS;

XX WPI; 2001-112438/12.

XX P-PSDB; AAB62775.

XX Novel human monoclonal antibody immunoreactive with human

PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1

PT in biological sample and providing passive immunotherapy to HIV-1

PT infected mammal.

XX Claim 4; Page 45; 81pp; English.

XX The present invention provides the protein and coding sequences for the
 CC variable regions of human monoclonal antibodies which are immunoreactive
 CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
 CC These can be used in diagnosis and therapy of HIV-1 infection

XX Sequence 360 BP; 73 A; 104 C; 107 G; 76 T; 0 U; 0 Other;

Query Match 78.5%; Score 268.4; DB 4; Length 360;

Best Local Similarity 88.6%; Pred. No. 1.3e-66;

Matches 303; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCGACGAGTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGACATGTCTCT 63

Db 19 GAGTCTGGCCGACGAGTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGACATGTCTCT 78

QY 64 GGTGGCTCCATCCGACGTGGTGTATTATTATTTGGAGTTGGGTCCGCCAGCCTCCAGGGAAG 123
 Db 79 GGTGGCTCCATCCGACGTGGTGTATTATTATTTGGAGTTGGGTCCGCCAGCCTCCAGGGAAG 138
 QY 124 GGCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTACAAACCCGTCCTC 183
 Db 139 GGCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTACAAACCCGTCCTC 198
 QY 184 AAGAGTCGAATTACCATGTTCAGTAGACACGCTCTAAGAACCATTTCTCCCTGAGACTGACC 243
 Db 199 AAGAGTCGAGTTACCATATCAGTAGACACGCTCTAAGAACCATTTCTCCCTGAGACTGAGC 258
 QY 244 TCTGTGACTCGCGGACACGGCCGCTATTACTGTGGCGGTGAGATGGGTACTATTG 300
 Db 259 TCTGTGACTCGCGGACACGGCCGCTATTACTGTGGCGGTGAGATGGGTACTATTG 318
 QY 301 TTGGACAACTGGGGCCAGGGAACCCCTGGTCACCGCTCTCCTCA 342
 Db 319 TTGACCCCTGGGGCCAGGGAACCCCTGGTCACCGCTCTCCTCA 360

RESULT 7

ADC99778

ID ADC99778 standard; DNA; 352 BP.

AC ADC99778;

XX 01-JAN-2004 (first entry)

XX Anti-human MUC18 antibody heavy chain variable domain DNA SEQ ID 7.

XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
 KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;
 KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
 KW lung cancer; human; ds; gene.

XX Homo sapiens.

XX WO2003057838-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041581.

XX 28-DEC-2001; 2001US-0346299P.

XX (ABGE-) ABGENIX INC.

XX Gudas J;

XX WPI; 2003-587113/55.

XX P-PSDB; ADC99776.

XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease
 PT or condition associated with expression of MUC18 in a patient, e.g.
 PT tumors, cancers, and other malignancies.

XX Claim 8; SEQ ID NO 7; 78pp; English.

XX The invention relates to a novel isolated monoclonal antibody comprising
 CC a heavy or light chain amino acid or a heavy or light chain variable
 CC domain where the antibody binds to MUC18. The monoclonal antibody of the
 CC invention demonstrates cytostatic activity and may be useful for treating
 CC a disease or condition associated with the expression of MUC18 on the
 CC cell surface such as tumours, specifically melanoma, oesophageal,
 CC pancreatic or colorectal tumours, carcinomas, particularly cervical
 CC carcinomas and cervical intraepithelial neoplasia and cancers including
 CC colorectal, breast or lung cancer, as well as other malignancies. The
 CC current sequence is that of the anti-human MUC18 monoclonal antibody
 CC heavy chain variable domain DNA of the invention.

XX Sequence 352 BP; 76 A; 102 C; 103 G; 71 T; 0 U; 0 Other;

Query Match 76.7%; Score 262.2; DB 9; Length 352;
Best Local Similarity 87.9%; Pred. No. 7.5e-65;
Matches 298; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

QY 4 GAGTGTGCCCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACCTGTCTCT 63
DB 16 GAGTGTGCCCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACCTGTCTCT 75

QY 64 GGTGCTCATCCGACGAGTGGTATTATTGGAGTTGGTCCGCGCAGCTCCAGGGAAG 123
DB 76 GGTGCTCATCCGACGAGTGGTATTATTGGAGTTGGTCCGCGCAGCTCCAGGGAAG 135

QY 124 GGCCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACCTACAAACCCGTCCTCTCA 183
DB 136 GGCCTGGAGTGGATGGGTACATCTATTACAGTGGAGACCTACTACACCCGTCCTCTCA 195

QY 184 AAGAGTCGAATTACCATGTCTAGTAGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 243
DB 196 AAGAGTCGAGTTACCATATCAGTAGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 255

QY 244 TCTGTGACTGCGCGGACACGCGCTCTATTACTGTGCGGTGAGATGGGTATCTTTG 303
DB 256 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGAG---AGGGGGAGATGGCTTAC 312

QY 304 GACAACTGGGCGCAGGGAACCTGTCTACCGTCTCTCTCA 342
DB 313 AAGTACTGGGCGCAGGGAACCTGTCTACCGTCTCTCTCA 351

RESULT 8
ADD05382
ID ADD05382 standard; DNA; 352 BP.
AC ADD05382;
DT 01-JAN-2004 (first entry)
DE Anti-MUC18 antibody heavy chain variable region DNA, SEQ ID No 7.
KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain;
KW gene; ds.
OS Homo sapiens.
PN WO2003057006-A2.
PD 17-JUL-2003.
PF 26-DEC-2002; 2002WO-US041582.
PR 28-DEC-2001; 2001US-0346460P.
XX (ABGE-) ABGENIX INC.
PI Gudas J, Bar-Eli M;
XX
DR WPI: 2003-577496/54.
DR P-PSDB; ADD05380.
XX
PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT associated with melanoma, or increasing survival of an animal having a
PT metastatic tumor.
XX
PS Disclosure; SEQ ID NO 7; 87pp; English.
XX
CC The invention relates to a novel monoclonal antibody used for inhibiting
CC tumour growth in an animal. The tumour inhibition process comprises
CC selecting an animal in need of treatment for a tumour, providing a
CC monoclonal antibody comprising a heavy chain amino acid, where the
CC antibody consists of any one of 10 fully defined sequences of 117-123

CC amino acids given in the specification, and where the monoclonal antibody
CC binds MUC18, and contacting the tumour with the antibody resulting in
CC inhibited proliferation of the cells. The monoclonal antibody has
CC cytotatic and can be used in the production of a vaccine. The monoclonal
CC antibodies against the MUC18 antigen are useful for diagnosing and
CC treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
CC increasing survival of an animal having a metastatic tumour. This
CC polynucleotide sequence represents the DNA encoding an anti-MUC18
CC antibody heavy chain, variable region, protein of the invention.
XX

SQ Sequence 352 BP; 76 A; 102 C; 103 G; 71 T; 0 U; 0 Other;

Query Match 76.7%; Score 262.2; DB 9; Length 352;
Best Local Similarity 87.9%; Pred. No. 7.5e-65;
Matches 298; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

QY 4 GAGTGTGCCCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACCTGTCTCT 63
DB 16 GAGTGTGCCCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACCTGTCTCT 75

QY 64 GGTGCTCATCCGACGAGTGGTATTATTGGAGTTGGTCCGCGCAGCTCCAGGGAAG 123
DB 76 GGTGCTCATCCGACGAGTGGTATTATTGGAGTTGGTCCGCGCAGCTCCAGGGAAG 135

QY 124 GGCCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACCTACAAACCCGTCCTCTCA 183
DB 136 GGCCTGGAGTGGATGGGTACATCTATTACAGTGGAGACCTACTACACCCGTCCTCTCA 195

QY 184 AAGAGTCGAATTACCATGTCTAGTAGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 243
DB 196 AAGAGTCGAGTTACCATATCAGTAGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 255

QY 244 TCTGTGACTGCGCGGACACGCGCTCTATTACTGTGCGGTGAGATGGGTATCTTTG 303
DB 256 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGAG---AGGGGGAGATGGCTTAC 312

QY 304 GACAACTGGGCGCAGGGAACCTGTCTACCGTCTCTCTCA 342
DB 313 AAGTACTGGGCGCAGGGAACCTGTCTACCGTCTCTCTCA 351

RESULT 9
ADC99798
ID ADC99798 standard; DNA; 358 BP.
AC ADC99798;
DT 01-JAN-2004 (first entry)
DE Anti-human MUC18 antibody heavy chain variable domain DNA SEQ ID 27.
XX
KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
KW lung cancer; human; ds; gene.
OS Homo sapiens.
XX
PN WO2003057838-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041581.
XX
PR 28-DEC-2001; 2001US-0346299P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J;
XX
DR WPI: 2003-587113/55.
DR P-PSDB; ADC99796.

```
XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease
PT or condition associated with expression of MUC18 in a patient, e.g.
PT tumors, cancers, and other malignancies.
XX
XX Claim 8; SEQ ID NO 27; 78pp; English.
XX
XX The invention relates to a novel isolated monoclonal antibody comprising
CC a heavy or light chain amino acid or a heavy or light chain variable
CC domain where the antibody binds to MUC18. The monoclonal antibody of the
CC invention demonstrates cytostatic activity and may be useful for treating
CC a disease or condition associated with the expression of MUC18 on the
CC cell surface such as tumours, specifically melanoma, oesophageal,
CC pancreatic or colorectal tumours, carcinomas, particularly cervical
CC carcinomas and cervical intraepithelial neoplasia and cancers including
CC colorectal, breast or lung cancer, as well as other malignancies. The
CC current sequence is that of the anti-human MUC18 monoclonal antibody
CC heavy chain variable domain DNA of the invention.
XX
XX Sequence 358 BP; 77 A; 103 C; 101 G; 77 T; 0 U; 0 Other;
XX
XX Query Match 76.1%; Score 260.4; DB 9; Length 358;
XX Best Local Similarity 87.1%; Pred. No. 2.4e-64;
XX Matches 298; Conservative 0; Mismatches 41; Indels 3; Gaps 1;
XX
XX 4 GAGTCTGGCCAGGACTGGTGAAGCTTTCACAGACCCTGTCCCTCAGCTGCTCTCT 63
XX 16 GAGTGGGGCCAGGACTGGTGAAGCTTTCACAGACCCTGTCCCTCAGCTGCTCTCT 75
XX
XX 64 GGTGGCTCCATCCGACGTGGTGGTATTATTGGAGTTGGTCCGCCAGCTCCAGGGAAG 123
XX 76 GGTGGCTCCATCAACAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 135
XX
XX 124 GGCTGGAGTGGATTCGCAACATCTATCAAGTGGCAACACCTACAAACCCGTCCTC 183
XX 136 GGCTGGAGTGGATTCGCAACATCTATCAAGTGGCAACACCTACAAACCCGTCCTC 195
XX
XX 184 AAGAGTCGAATTACCATGTTCAGTAGACAGCTCTAAGAACACCTTCTCCCTGAGACTGACC 243
XX 196 AAGAGTCGAATTACCATGTTCAGTAGACAGCTCTAAGAACACCTTCTCCCTGAGACTGACC 255
XX
XX 244 TCTGTGACTGCGCGGACACGGCGCTCTATTACTGTGCGCG---GTCAGATGGGTACT 300
XX 256 TCTATGACTGCGCGGACACGGCGCTGTATTACTGTGCGGAGATCGGGAACAGCTGGT 315
XX
XX 301 TTGGACAACCTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342
XX 316 TTTGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 357
XX
XX RESULT 10
XX ADD05402
XX ID ADD05402 standard; DNA; 358 BP.
XX
XX AC ADD05402;
XX
XX XX Homo sapiens.
XX PN WO2003057006-A2.
XX XX
XX PD 17-JUL-2003.
XX
XX XX 26-DEC-2002; 2002WO-US041582.
XX XX
XX XX 28-DEC-2001; 2001US-0346460P.
XX XX
XX PR Anti-MUC18 antibody heavy chain variable region DNA, SEQ ID NO 27.
XX
XX monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
XX antigen; tumour metastasis; melanoma; metastatic; human; heavy chain;
XX gene; ds.
XX
XX OS Homo sapiens.
XX OS
XX XX WO2003057006-A2.
XX PN
XX XX
XX PD 17-JUL-2003.
XX
XX XX 26-DEC-2002; 2002WO-US041582.
XX XX
XX XX 28-DEC-2001; 2001US-0346460P.
XX XX
XX PR
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XX (ABGE-) ABGENIX INC.
XX PA
XX PI Gudas J, Bar-Eli M;
XX DR WPI; 2003-577496/54.
XX DR P-PSDB; ADD05400.
XX
XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT associated with melanoma, or increasing survival of an animal having a
PT metastatic tumor.
XX
XX Disclosure; SEQ ID NO 27; 87pp; English.
XX
XX The invention relates to a novel monoclonal antibody used for inhibiting
CC tumour growth in an animal. The tumour inhibition process comprises
CC selecting an animal in need of treatment for a tumour, providing a
CC monoclonal antibody comprising a heavy chain amino acid, where the
CC antibody consists of any one of 10 fully defined sequences of 117-123
CC amino acids given in the specification, and where the monoclonal antibody
CC binds MUC18, and contacting the tumour with the antibody resulting in
CC inhibited proliferation of the cells. The monoclonal antibody has
CC cytostatic and can be used in the production of a vaccine. The monoclonal
CC antibodies against the MUC18 antigen are useful for diagnosing and
CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
CC increasing survival of an animal having a metastatic tumour. This
CC polynucleotide sequence represents the DNA encoding an anti-MUC18
CC antibody heavy chain, variable region, protein of the invention.
XX
XX Sequence 358 BP; 77 A; 103 C; 101 G; 77 T; 0 U; 0 Other;
XX
XX Query Match 76.1%; Score 260.4; DB 9; Length 358;
XX Best Local Similarity 87.1%; Pred. No. 2.4e-64;
XX Matches 298; Conservative 0; Mismatches 41; Indels 3; Gaps 1;
XX
XX 4 GAGTCTGGCCAGGACTGGTGAAGCTTTCACAGACCCTGTCCCTCAGCTGCTCTCT 63
XX 16 GAGTGGGGCCAGGACTGGTGAAGCTTTCACAGACCCTGTCCCTCAGCTGCTCTCT 75
XX
XX 64 GGTGGCTCCATCCGACGTGGTGGTATTATTGGAGTTGGTCCGCCAGCTCCAGGGAAG 123
XX 76 GGTGGCTCCATCAACAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 135
XX
XX 124 GGCTGGAGTGGATTCGCAACATCTATCAAGTGGCAACACCTACAAACCCGTCCTC 183
XX 136 GGCTGGAGTGGATTCGCAACATCTATCAAGTGGCAACACCTACAAACCCGTCCTC 195
XX
XX 184 AAGAGTCGAATTACCATGTTCAGTAGACAGCTCTAAGAACACCTTCTCCCTGAGACTGACC 243
XX 196 AAGAGTCGAATTACCATGTTCAGTAGACAGCTCTAAGAACACCTTCTCCCTGAGACTGACC 255
XX
XX 244 TCTGTGACTGCGCGGACACGGCGCTCTATTACTGTGCGCG---GTCAGATGGGTACT 300
XX 256 TCTATGACTGCGCGGACACGGCGCTGTATTACTGTGCGGAGATCGGGAACAGCTGGT 315
XX
XX 301 TTGGACAACCTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342
XX 316 TTTGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 357
XX
XX RESULT 11
XX AAF29046
XX ID AAF29046 standard; DNA; 369 BP.
XX
XX AC AAF29046;
XX
XX XX Homo sapiens.
XX PN WO2003057006-A2.
XX XX
XX PD 03-APR-2001 (first entry)
XX
XX XX Human HIV-1 monoclonal antibody coding sequence SEQ ID NO: 2.
XX XX
XX XX Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
```

KW envelope glycoprotein; gp120; diagnosis; ds.

XX Homo sapiens.

PN WO200100678-A1.

PD 04-JAN-2001.

XX 23-JUN-2000; 2000WO-US017327.

XX 30-JUN-1999; 99US-0141701P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Watkins BA, Reitz MS;

XX WPI; 2001-112438/12.

DR P-PSDB; AAB62745.

XX Novel human monoclonal antibody immunoreactive with human
PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
PT in biological sample and providing passive immunotherapy to HIV-1
PT infected mammal.

XX Claim 4; Page 34-35; 81pp; English.

XX The present invention provides the protein and coding sequences for the
CC variable regions of human monoclonal antibodies which are immunoreactive
CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
CC These can be used in diagnosis and therapy of HIV-1 infection

XX SQ Sequence 369 BP; 75 A; 104 C; 107 G; 83 T; 0 U; 0 Other;

Query Match 75.4%; Score 257.8; DB 4; Length 369;

Best Local Similarity 86.0%; Pred. No. 1.4e-63;

Matches 302; Conservative 0; Mismatches 37; Indels 12; Gaps 1;

QY 4 GAGTGTGCGCCAGGACTGGTGAAGCCTTCACAGACCCCTGCTCCCTCAGCTGCTCTCT 63

Db 19 GAGTGTGCGCCAGGACTGGTGAAGCCTTCACAGACCCCTGCTCCCTCAGCTGCTCTCT 78

QY 64 GTGTGCTCATCCGAGTGGTGGTATTATTGGAGTGGTCCGCGAGCTCCAGGGAAG 123

Db 79 GTGTGCTCATCCGAGTGGTGGTATTATTGGAGTGGTCCGCGAGCTCCAGGGAAG 138

QY 124 GSCCTGGAGTGATCGGCAACATCTATCAGCTGGCAACCTACAAACCCGTCCTC 183

Db 139 GSCCTGGAGTGATCGGCAACATCTATCAGCTGGCAACCTACAAACCCGTCCTC 198

QY 184 AAGAGTCGAATTACCATGTCTAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGACTGACC 243

Db 199 AAGAGTCGAATTACCATGTCTAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGACTGACC 258

QY 244 TCTGTGACTGCGCGGACACGGCCGTCTATTACTGTGCGGGTC-----AGAT 291

Db 259 TCTGTGACTGCGCGGACACGGCCGTCTATTACTGTGCGGGCCGCGTATTGTGGTGT 318

QY 292 GGGTATATTGGCAACTTGGGCGCAGGGAACCCCTGTCACCGTCTCTCTCA 342

Db 319 GATTGCTCTTTGACTACTGGGCGCAGGGAACCCCTGTCACCGTCTCTCTCA 369

RESULT 12

ID ADC99806

XX ADC99806 standard; DNA; 352 BP.

AC ADC99806;

XX 01-JAN-2004 (first entry)

XX Anti-human MUC18 antibody heavy chain variable domain DNA SEQ ID 35.

XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;

KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
KW lung cancer; human; ds; gene.

XX Homo sapiens.

XX WO2003057838-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041581.

XX 28-DEC-2001; 2001US-0346299P.

XX (ABGE-) ABGENIX INC.

XX Gudas J;

XX WPI; 2003-587113/55.

DR P-PSDB; ADC99804.

XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease
PT or condition associated with expression of MUC18 in a patient, e.g.
PT tumors, cancers, and other malignancies.

XX Claim 8; SEQ ID NO 35; 78pp; English.

XX The invention relates to a novel isolated monoclonal antibody comprising
CC a heavy or light chain amino acid or a heavy or light chain variable
CC domain where the antibody binds to MUC18. The monoclonal antibody of the
CC invention demonstrates cytostatic activity and may be useful for treating
CC a disease or condition associated with the expression of MUC18 on the
CC cell surface such as tumours, specifically melanoma, oesophageal,
CC pancreatic or colorectal tumours, carcinomas, particularly cervical
CC carcinomas and cervical intraepithelial neoplasia and cancers including
CC colorectal, breast or lung cancer, as well as other malignancies. The
CC current sequence is that of the anti-human MUC18 monoclonal antibody
CC heavy chain variable domain DNA of the invention.

XX SQ Sequence 352 BP; 77 A; 101 C; 105 G; 69 T; 0 U; 0 Other;

Query Match 74.5%; Score 254.8; DB 9; Length 352;

Best Local Similarity 86.7%; Pred. No. 9.6e-63;

Matches 293; Conservative 0; Mismatches 42; Indels 3; Gaps 1;

QY 5 AGTGTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGCTCCCTCAGCTGCTCTCTG 64

Db 17 AGTGTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGCTCCCTCAGCTGCTCTCTG 76

QY 65 GTGGCTCCATCCGAGTGGTGGTATTATTGGAGTGGTCCGCGAGCTCCAGGGAAGG 124

Db 77 GTGGCTCCATCCGAGTGGTGGTATTATTGGAGTGGTCCGCGAGCTCCAGGGAAGG 136

QY 125 GCCTGGAGTGGATCGGCAACATCTATCAGCTGGCAACACCTACAAACCCGTCCTCTCA 184

Db 137 GCCTGGAGTGGATCGGCAACATCTATCAGCTGGCAACACCTACAAACCCGTCCTCTCA 196

QY 185 AGAGTCGAATTACCATGTCTAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGACTGAGCT 244

Db 197 AGAGTCGAATTACCATGTCTAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGACTGAGCT 256

QY 245 CTGTGACTGCGCGGACACGGCCGTCTATTACTGTGCGGCTCAGATGGGTATATCTTGG 304

Db 257 CTGTGACTGCGCGGACACGGCCGTCTATTACTGTGCGGCTCAGATGGGTATATCTTGG 313

QY 305 ACAACTGGGCGCAGGGAACCCCTGTCACCGTCTCTCTCA 342

Db 314 GATACTGGGCGCAGGGAACCCCTGTCACCGTCTCTCTCA 351

RESULT 13

ID ADD05410

XX ADD05410 standard; DNA; 352 BP.

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XX AC ADD05410;
XX DT 01-JAN-2004 (first entry)
XX DE Anti-MUC18 antibody heavy chain variable region DNA, SEQ ID NO 35.
XX KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
XX KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain;
XX KW gene; ds.
XX OS Homo sapiens.
XX PN WO2003057006-A2.
XX PD 17-JUN-2003.
XX PF 26-DEC-2002; 2002WO-US041582.
XX PR 28-DEC-2001; 2001US-0346460P.
XX PA (ABGE-) ABGENIX INC.
XX PI Gudas J, Bar-Eli M;
XX DR WPI; 2003-577496/54.
XX DR P-PSDB; ADD05408.
XX PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
XX PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
XX PT associated with melanoma, or increasing survival of an animal having a
XX PT metastatic tumor.
XX PS Disclosure; SEQ ID NO 35; 87pp; English.
XX PI
XX CC The invention relates to a novel monoclonal antibody used for inhibiting
XX CC tumour growth in an animal. The tumour inhibition process comprises
XX CC selecting an animal in need of treatment for a tumour, providing a
XX CC monoclonal antibody comprising a heavy chain amino acid, where the
XX CC antibody consists of any one of 10 fully defined sequences of 117-123
XX CC amino acids given in the specification, and where the monoclonal antibody
XX CC binds MUC18, and contacting the tumour with the antibody resulting in
XX CC inhibited proliferation of the cells. The monoclonal antibody has
XX CC cytostatic and can be used in the production of a vaccine. The monoclonal
XX CC antibodies against the MUC18 antigen are useful for diagnosing and
XX CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or
XX CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
XX CC increasing survival of an animal having a metastatic tumour. This
XX CC polynucleotide sequence represents the DNA encoding an anti-MUC18
XX CC antibody heavy chain, variable region, protein of the invention.
XX SQ Sequence 352 BP; 77 A; 101 C; 105 G; 69 T; 0 U; 0 Other;

Query Match 74.5%; Score 254.8; DB 9; Length 352;
Best Local Similarity 86.7%; Pred. No. 9.6e-63;
Matches 293; Conservative 0; Mismatches 42; Indels 3; Gaps 1;

Qy 5 AGCTGGCCAGGACTGGTGAAGCTTCACAGACCTGTCCTCCTCAGCTGCTCTCTG 64
Db 17 AGTCGGGCCAGGACTGGTGAAGCTTCAGAGACCTGTCCTCCTCAGCTGCTCTCTG 76
Qy 65 GTGGCTCCATCCGAGTGGTGGTTATTATTGGAGTTGGTCCGCGAGCTCCAGGGAAG 124
Db 77 GTGGCTCCATCAGCAGTGGTACTTACCACTGGAGCTGGATCCGCGAGCACCAGGAGGG 136
Qy 125 GCCTGGAGTGGATCGGCAACATCTATACAGTGGCAACACCTACAAACCCGTCCTCA 184
Db 137 GCCTGGAGTGGATGATACATCTATTACAGTGGGAGCACCTACCAACCCGTCCTCA 196
Qy 185 AGAGTCGAATTACCATGTCAGTACACGCTTAGAACCACTTCTCCCTGAGACTGACCT 244
Db 197 AGAGTCGAATTACCATATACATACAGTACACGCTTAGAACCACTTCTCCCTGAGACTGAGCT 256

245 CTGTGACTGCGCGGCACACGGCCGCTCTATTACTGTGCGGTGATGGGTATCTTTGG 304
257 CTGTGACGGCGCGGCACACGGCCGCTGTATTACTGTGCGAG--AGGGGAGATGGCTACA 313
305 ACAACTGGGCGCAGGGAACCTGTGTACCGCTCTCTCTCA 342
314 GATACTGGGCGCAGGGAACCTGTGTACCGCTCTCTCTCA 351

RESULT 14
AAF29066
ID AAF29066 standard; DNA; 366 BP.
XX AC AAF29066;
XX DT 03-APR-2001 (first entry)
XX DE Human HIV-1 monoclonal antibody coding sequence SEQ ID NO: 22.
XX KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
XX KW envelope glycoprotein; gp120; diagnosis; ds.
XX OS Homo sapiens.
XX PN WO200100678-A1.
XX PD 04-JAN-2001.
XX PF 23-JUN-2000; 2000WO-US017327.
XX PR 30-JUN-1999; 99US-0141701P.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Watkins BA, Reitz MS;
XX DR WPI; 2001-112438/12.
XX DR P-PSDB; AAB62765.
XX PT Novel human monoclonal antibody immunoreactive with human
XX PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
XX PT in biological sample and providing passive immunotherapy to HIV-1
XX PT infected mammal.
XX PS Claim 4; Page 42; 81pp; English.
XX CC The present invention provides the protein and coding sequences for the
XX CC variable regions of human monoclonal antibodies which are immunoreactive
XX CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
XX CC These can be used in diagnosis and therapy of HIV-1 infection
XX SQ Sequence 366 BP; 73 A; 107 C; 106 G; 80 T; 0 U; 0 Other;

Query Match 73.5%; Score 251.2; DB 4; Length 366;
Best Local Similarity 85.1%; Pred. No. 1e-61;
Matches 296; Conservative 0; Mismatches 43; Indels 9; Gaps 1;

Qy 4 GAGTCTGGCCAGGACTGGTGAAGCTTCACAGACCTTCACCTGTCCTCCTCAGCTGCTCT 63
Db 19 GAGTCGGGCCAGGACTGGTGAAGCTTCACAGACCTTCACCTGTCCTCCTCAGCTGCTCT 78
Qy 64 GGTGGCTCCATCCGACGTGGTGGTTATTATTGGAGTTGGTCCGCGAGCTCCAGGGAAG 123
Db 79 GGTGGCTCCATCCGACGTGGTGGTTATTATTGGAGTTGGTCCGCGAGCTCCAGGGAAG 138
Qy 124 GGCTGGAGTGGATCGGCAACATCTATACAGTGGCAACACCTACAAACCCGTCCTC 183
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Qy 184 AAGAGTCGAATTACCATGTCAGTAGACACGCTTAGAACCACTTCTCCCTGAGACTGACC 243
Db 199 AAGAGTCGAATTACCATATACATACAGTAGACACGCTTAGAACCACTTCTCCCTGAGACTGAGC 258
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OY 295 TATACTTTGGACAACCTGGGCGGACAGGAAACCCCTGGTCAACCGTCTCTCTCA 342
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Db 319 ACTGGACTGTGCTACTGTGGGCGGTGCGACCCCTGGTCACTGTCTCTCTCA 366
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RESULT 15
AAA46876
ID AAA46876 standard; DNA; 516 BP.
XX
AC AAA46876;
XX
DT 03-OCT-2000 (first entry)
XX
DE DNA encoding the heavy chain of immunoglobulin clone 2.1.1.3.
XX
KW Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
KW proliferative disorder; cancer; immunodeficient disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200037504-A2.
XX
PD 29-JUN-2000.
XX
PF 23-DEC-1999; 99WO-US030895.
XX
PR 23-DEC-1998; 98US-0113647P.
XX
PA (PRIZ ) PRIZER INC.
PA (ABGE-) ABGENIX INC.
XX
PI Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
PI Corvalan JR;
XX
DR WPI: 2000-442647/38.
DR P-PSDB; AAY93713.
XX
PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)
PT -4 containing specified heavy and light chain sequences, useful for
PT treating, e.g. immune disorders.
XX
PS Example 2; Fig 1G; 157pp; English.
XX
CC The present sequence encodes a heavy chain of an antibody of the
CC invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)
CC -4. Antibodies of the invention are composed of a heavy chain variable
CC region, comprising a modified contiguous sequence from a PRL-PR3 sequence
CC encoded by a human VH3-33 family gene. The modifications are contained in
CC CDRI, CDRI2 and/or framework regions. The antibodies may be used to
CC inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
CC disorders (e.g. autoimmune disease, diabetes and graft rejection) and
CC proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
CC used to up-regulate immune system to up-regulate immunodeficient
CC disorders
XX
SQ Sequence 516 BP; 103 A; 167 C; 142 G; 104 T; 0 U; 0 Other;
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Query Match 73.5%; Score 251.2; DB 3; Length 516;
Best Local Similarity 85.7%; Pred. No. 1.1e-61;
Matches 293; Conservative 0; Mismatches 43; Indels 6; Gaps 1;

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Db 1 TCGGGCCAGGACTGGTGAAGCTTCACAGATCCTGTCCCTCACCTGCACTCTCTCTGT 60
|||
OY 67 GGTCCATCCGAGTGGTGTATTATTGGAGTGGGTCGCGCAGCTCCAGGGAAGGSC 126
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Db 61 GGCTCCATCAGCAGTGGTGGTCTACTACTGAGCTGGATCCGCCAGCACCAGGGAAGGSC 120
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OY 127 CTGGAGTGGATCGGCAACATCTTATCACAGTGGCAACACCTACAAACCCGTCCTCAAG 186
|||
Db 121 CTGGAGTGGATGGGTACATCTATTACATTGGGAACACTACTACAAACCCGTCCTCAAG 180
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OY 187 AGTCGAATTACCATGTCACTCAGTAGACACAGTCTAAGAACCCACTTCTCCCTGAGACTGACCTCT 246
|||
Db 181 AGTCGAGTTACCATATATCAGTAGACACAGTCTAAGAACCCAGTTCTCCCTGAAGCTGAGCTCT 240
|||
OY 247 GTGACTGGCGGGGACACCGCCGCTCTATTACTGTGCGCGGTCAAGTGGG-----TATACT 300
|||
Db 241 GTGACTGGCGGGGACACCGCCGCTGTATTATTGTGGGAGAGATAGTGGGAGACTACTACGCT 300
|||
OY 301 TTGGACAACCTGGGGCCAGGGAAACCCCTGGTCAACCGTCTCTCTCA 342
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Db 301 ATAGACGCTCTGGGGCCAGGGACACCGGTCAACCGTCTCTCTCA 342
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-10-027-725A-2

Perfect score: 342

Sequence: 1 ctgagctgtgcccaggact.....ccctgtaccgtctctca 342

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3225727 seqs, 2453303834 residues

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Maximum Match 100%

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Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	342	100.0	342	15	US-10-027-725A-2
2	324.4	94.9	342	15	US-10-027-725A-3
3	298.8	87.4	342	15	US-10-027-725A-1
4	271.8	79.5	352	15	US-10-330-613-15
5	271.8	79.5	352	15	US-10-330-613-15
6	271.8	79.5	352	17	US-10-660-357-15
7	262.2	76.7	352	15	US-10-330-613-7
8	262.2	76.7	352	15	US-10-330-530-7
9	262.2	76.7	352	17	US-10-660-357-7
10	261.4	76.4	663	10	US-09-972-656-79
11	260.4	76.1	358	15	US-10-330-613-27
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13	260.4	76.1	358	17	US-10-660-357-27
14	256.4	75.0	370	16	US-10-309-762-186
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					Sequence 3, Appli
					Sequence 1, Appli
					Sequence 15, Appl
					Sequence 15, Appl
					Sequence 7, Appli
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					Sequence 79, Appl
					Sequence 27, Appl
					Sequence 27, Appl
					Sequence 27, Appl
					Sequence 186, App

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16	254.8	74.5	352	15	US-10-330-613-35	Sequence 35, Appl
17	254.8	74.5	352	15	US-10-330-530-35	Sequence 35, Appl
18	254.8	74.5	352	17	US-10-660-357-35	Sequence 35, Appl
19	252.6	73.9	361	16	US-10-309-762-191	Sequence 191, App
20	251.6	73.6	370	16	US-10-309-762-189	Sequence 189, App
21	250.6	73.3	370	16	US-10-309-762-185	Sequence 185, App
22	250.4	73.2	376	16	US-10-309-762-187	Sequence 187, App
23	249.4	72.9	352	16	US-10-309-762-203	Sequence 203, App
24	248.8	72.7	376	16	US-10-309-762-184	Sequence 184, App
25	248.8	72.7	376	16	US-10-309-762-197	Sequence 197, App
26	248.8	72.7	376	16	US-10-309-762-199	Sequence 199, App
27	248.4	72.6	519	16	US-10-309-762-174	Sequence 174, App
28	248.2	72.6	367	16	US-10-309-762-195	Sequence 195, App
29	245.2	71.7	370	16	US-10-309-762-200	Sequence 200, App
30	244.6	71.5	361	16	US-10-309-762-193	Sequence 193, App
31	244.2	71.4	381	17	US-10-312-316-66	Sequence 66, Appl
32	244.2	71.4	382	16	US-10-309-762-194	Sequence 194, App
33	244	71.3	378	9	US-09-974-449-5	Sequence 5, Appli
34	243	71.1	450	15	US-10-390-986-13	Sequence 13, Appl
35	242.6	70.9	324	9	US-09-864-761-31244	Sequence 31244, A
36	240.4	70.3	370	16	US-10-309-762-201	Sequence 201, App
37	240.4	70.3	370	16	US-10-309-762-212	Sequence 212, App
38	239.4	70.0	384	17	US-10-312-316-68	Sequence 68, Appl
39	239.2	69.9	393	9	US-09-925-299-198	Sequence 198, App
40	239.2	69.9	393	10	US-09-925-299-198	Sequence 198, App
41	237.8	69.5	381	17	US-10-312-316-64	Sequence 64, Appl
42	234.6	68.6	1543	9	US-09-800-729-74	Sequence 74, Appl
43	231.2	67.6	417	9	US-09-905-243-7	Sequence 41, Appl
44	231	67.5	360	13	US-10-371-942-41	Sequence 2, Appli
45	230.6	67.4	349	12	US-10-269-711-2	

ALIGNMENTS

RESULT 1

US-10-027-725A-2
; Sequence 2, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-027-725A-2

Query Match 100.0%; Score 342; DB 15; Length 342;
Best Local Similarity 100.0%; Pred. No. 4.6e-104;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CTCGAGTCTGCCAGGACCTGGTGAAGCCCTTCACAGACCTGCTCCCTCACTGCATGTC	60
Db	1	CTCGAGTCTGCCAGGACCTGGTGAAGCCCTTCACAGACCTGCTCCCTCACTGCATGTC	60
Qy	61	TCCTGGTGGCTCCATCCCGACGTGGTGTATTATTGGAGTTGGGTCCGCCACCTCCAGGG	120
Db	61	TCCTGGTGGCTCCATCCCGACGTGGTGTATTATTGGAGTTGGGTCCGCCACCTCCAGGG	120
Qy	121	AAGGCGCTGGAGTGGATTCGGCAACATCTATCAGTGGCAACACCTACACCAACCCCTCC	180
Db	121	AAGGCGCTGGAGTGGATTCGGCAACATCTATCAGTGGCAACACCTACACCAACCCCTCC	180
Qy	181	CTCAGAGTCCGAATTACCATGTCTAGTAGACACGCTCTAAGAACCACTTCTCCCTGAGATG	240

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RESULT 2

US-10-027-725A-3

; Sequence 3, Application US/10027725A

; Publication No. US20030082659A1

; GENERAL INFORMATION:

; APPLICANT: Flicker, Sabine

; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof

; FILE REFERENCE: 25401-4

; CURRENT APPLICATION NUMBER: US/10/027,725A

; PRIOR FILING DATE: 2002-08-09

; PRIOR APPLICATION NUMBER: US 60/259,436

; PRIOR FILING DATE: 2000-12-29

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 342

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-027-725A-3

Query Match 94.9%; Score 324.4; DB 15; Length 342;
Best Local Similarity 96.8%; Pred. No. 3.6e-98;
Matches 331; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 CTCGAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACTGCACTGTC 60
Db 1 CTCGAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACTGCACTGTC 60
QY 61 TCTGTGCTCCATCCGAGTGGTGTATTATTGAGTTGGTTCGGCAGCCTCCAGG 120
Db 61 TCTGTGCTCCATCCGAGTGGTGTATTATTGAGTTGGTTCGGCAGCCTCCAGG 120
QY 121 AAGGCCCTGGAGTGGTGAACATCTATCAGTGGCAACACCTACAAACCCGTC 180
Db 121 AAGGCCCTGGAGTGGTGAACATCTATCAGTGGCAACACCTACAAACCCGTC 180
QY 181 CTCAGAGTCGAATTAACATGTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGACTG 240
Db 181 CTCAGAGTCGAATTAACATGTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGACTG 240
QY 241 ACCTCTGTGACTGCCGCGACAGCGCCGCTATTACTGTGCGGTCAGATGGGTATCT 300
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QY 301 TTGGACAACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342
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RESULT 3

US-10-027-725A-1

; Sequence 1, Application US/10027725A

; Publication No. US20030082659A1

; GENERAL INFORMATION:

; APPLICANT: Flicker, Sabine

; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof

; FILE REFERENCE: 25401-4

; CURRENT APPLICATION NUMBER: US/10/027,725A

; PRIOR FILING DATE: 2002-08-09

; PRIOR APPLICATION NUMBER: US 60/259,436

; PRIOR FILING DATE: 2000-12-29

; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1

; LENGTH: 342

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-027-725A-1

Query Match 87.4%; Score 298.8; DB 15; Length 342;
Best Local Similarity 92.1%; Pred. No. 1.3e-89;
Matches 315; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1 CTCGAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACTGCACTGTC 60
Db 1 CTCGAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACTGCACTGTC 60
QY 61 TCTGTGCTCCATCCGAGTGGTGTATTATTGAGTTGGTTCGGCAGCCTCCAGG 120
Db 61 TCTGTGCTCCATCCGAGTGGTGTATTATTGAGTTGGTTCGGCAGCCTCCAGG 120
QY 121 AAGGCCCTGGAGTGGTGAACATCTATCAGTGGCAACACCTACAAACCCGTC 180
Db 121 AAGGCCCTGGAGTGGTGAACATCTATCAGTGGCAACACCTACAAACCCGTC 180
QY 181 CTCAGAGTCGAATTAACATGTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGACTG 240
Db 181 CTCAGAGTCGAATTAACATGTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGACTG 240
QY 241 ACCTCTGTGACTGCCGCGACAGCGCCGCTATTACTGTGCGGTCAGATGGGTATCT 300
Db 241 ACCTCTGTGACTGCCGCGACAGCGCCGCTATTACTGTGCGGTCAGATGGGTATCT 300
QY 301 TTGGACAACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342
Db 301 TTGGACAACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342

RESULT 4

US-10-330-613-15

; Sequence 15, Application US/10330613

; Publication No. US20030147809A1

; GENERAL INFORMATION:

; APPLICANT: Gudas, Jean

; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN

; FILE REFERENCE: ABGENIX 022A

; CURRENT APPLICATION NUMBER: US/10/330,613

; CURRENT FILING DATE: 2002-12-26

; PRIOR APPLICATION NUMBER: 60/346299

; PRIOR FILING DATE: 2001-12-18

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 15

; LENGTH: 352

; TYPE: DNA

; ORGANISM: Homo Sapiens

US-10-330-613-15

Query Match 79.5%; Score 271.8; DB 15; Length 352;
Best Local Similarity 89.7%; Pred. No. 1.5e-80;
Matches 304; Conservative 0; Mismatches 32; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACTGCACTGTCCT 63
Db 16 GAGTGGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACTGCACTGTCCT 75
QY 64 GGTGGCTCCATCCGAGTGGTGTATTATTGAGTTGGTTCGGCAGCCTCCAGGGAAG 123
Db 76 GGTGGCTCCATCAGCAGTGGTGGTTACTACTGAGCTTGGATCCGCGCAGCACCCAGGGAAG 135
QY 124 GGCCTGGAGTGGATCGGCAACATCTATCAGAGTGGCAACACCTACAAACCCGTCCTC 183
Db 136 GGCCTGGAGTGGATCGGCAACATCTATCAGAGTGGCAACACCTACTACAAACCCGTCCTC 195

Db 136 GGCCTGGAGTGAATGGGTACATCTATTACAGTGGGAGCACCTACTACAAACCGTCCCTC 195
QY 184 AAGAGTCGAATACCATGTCACTAGACAGCTCTTAAGAACCACTTCTCCCTGAGACTGACC 243
Db 196 AAGAGTCGAGTTACCATATACATAGACAGCTTAAGAACCACTTCTCCCTGAGCTGAGC 255
QY 244 TCTGTGACTGCGCGGACACGCGCGTCTATTACTGTGCGCGTCAAGTGGGTATACTTTG 303
Db 256 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGGAG---AGGGGGAGATGGCTAC 312
QY 304 GACAACTGGGCGGACAGGACCTGTGTACCGTCTCTCTCA 342
Db 313 AAGTACTGGGCGGACAGGACCTGTGTACCGTCTCTCTCA 351

RESULT 8

US-10-330-530-7

; Sequence 7, Application US/10330530

; Publication No. US20030152514A1

; GENERAL INFORMATION:

; APPLICANT: Gudas, Jean

; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES

; FILE REFERENCE: ABGENIX.031A

; CURRENT APPLICATION NUMBER: US/10/330,530

; PRIOR FILING DATE: 2002-12-26

; PRIOR FILING DATE: 2001-12-26

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7

; LENGTH: 352

; TYPE: DNA

; ORGANISM: Homo Sapiens

US-10-330-530-7

Query Match 76.7%; Score 262.2; DB 15; Length 352;
Best Local Similarity 87.9%; Pred. No. 2.4e-77;
Matches 298; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

QY 4 GAGTCTGCCGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACTGCTCTCT 63
Db 16 GAGTCTGCCGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACTGCTCTCT 75
QY 64 GGTGCTCCATCCGAGTGGTGGTTATTATTGGAGTTGGTCCGCGAGCCTCCAGGGAG 123
Db 76 GGTGCTCCATCCAGCAGTGGTACTATCCACTGGAGTGGATCCGCGACACCCAGGGAG 135
QY 124 GGCCTGGAGTGGATCGGCAACATCTATCAGTGGCAACACTACAAACCCGTCCTC 183
Db 136 GGCCTGGAGTGGATGGGTACATCTATTACAGTGGGAGCACCCTACTACAAACCCGTCCTC 195
QY 184 AAGAGTCGAATACCATGTCACTAGACAGCTTAAGAACCACTTCTCCCTGAGACTGACC 243
Db 196 AAGAGTCGAGTTACCATATACATAGACAGCTTAAGAACCACTTCTCCCTGAGCTGAGC 255
QY 244 TCTGTGACTGCGCGGACACGCGCGTCTATTACTGTGCGCGTCAAGTGGGTATACTTTG 303
Db 256 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGGAG---AGGGGGAGATGGCTAC 312
QY 304 GACAACTGGGCGGACAGGACCTGTGTACCGTCTCTCTCA 342
Db 313 AAGTACTGGGCGGACAGGACCTGTGTACCGTCTCTCTCA 351

RESULT 9

US-10-660-357-7

; Sequence 7, Application US/10660357

; Publication No. US20040115205A1

; GENERAL INFORMATION:

; APPLICANT: Bar-Eli, Menashe

; APPLICANT: Green, Lary L.

; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18

; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-660-357-7

Query Match 76.7%; Score 262.2; DB 17; Length 352;
Best Local Similarity 87.9%; Pred. No. 2.4e-77;
Matches 298; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

QY 4 GAGTCTGCCGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACTGCTCTCT 63
Db 16 GAGTCTGCCGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACTGCTCTCT 75
QY 64 GGTGCTCCATCCGAGTGGTGGTTATTATTGGAGTTGGTCCGCGAGCCTCCAGGGAG 123
Db 76 GGTGCTCCATCCAGCAGTGGTACTATCCACTGGAGTGGATCCGCGACACCCAGGGAG 135
QY 124 GGCCTGGAGTGGATCGGCAACATCTATCAGTGGCAACACTACAAACCCGTCCTC 183
Db 136 GGCCTGGAGTGGATGGGTACATCTATTACAGTGGGAGCACCCTACTACAAACCCGTCCTC 195
QY 184 AAGAGTCGAATACCATGTCACTAGACAGCTTAAGAACCACTTCTCCCTGAGACTGACC 243
Db 196 AAGAGTCGAGTTACCATATCAGTAGACAGCTTAAGAACCACTTCTCCCTGAGCTGACC 255
QY 244 TCTGTGACTGCGCGGACACGCGCGTCTATTACTGTGCGCGTCAAGTGGGTATACTTTG 303
Db 256 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGGAG---AGGGGGAGATGGCTAC 312
QY 304 GACAACTGGGCGGACAGGACCCCTGTGTACCGTCTCTCTCA 342
Db 313 AAGTACTGGGCGGACAGGACCCCTGTGTACCGTCTCTCTCA 351

RESULT 10

US-09-972-656-79

; Sequence 79, Application US/09972656

; Publication No. US20030099647A1

; GENERAL INFORMATION:

; APPLICANT: Deshpande, Rajendra

; APPLICANT: Tsai, Mei-Mei

; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma

; TITLE OF INVENTION: Neutralizing Activity

; FILE REFERENCE: A-799

; CURRENT APPLICATION NUMBER: US/09/972,656

; CURRENT FILING DATE: 2001-10-05

; NUMBER OF SEQ ID NOS: 135

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 79

; LENGTH: 663

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(663)

US-09-972-656-79

Query Match 76.4%; Score 261.4; DB 10; Length 663;
Best Local Similarity 86.3%; Pred. No. 5.3e-77;
Matches 289; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 4 GAGTCTGCCGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACTGCTCTCT 63
Db 16 GAGTCTGCCGCCAGGACTGGTGAAGCCTTCGAGAGACCCCTGTCCCTCACTGCGGTCTCT 75

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QY 64 GGTGGCTCCATCCGACGTGGTGTATTATTATGGAGTTGGTCCGCCAGCCTCCAGGGAAG 123
Db 76 GGTGGCTCCATCCGACGTGGTGTATTCTCTGGAGCTGGATCCGGCAGCCACACAGGGAAG 135
QY 124 GGCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTTCAACAACCCCGTCCCTC 183
Db 136 GGCTGGAGTGGATGGGTACATCTATCATAGTGGGAGCCTACTACAAACCCGTCCTC 195
QY 184 AAGAGTCGAATTACCATGTCTAGTAGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 243
Db 196 AAGAGTCGAGTCACCATATCAGTAGACAGGTCCAAAGAACAGATTCTCCCTGAAGCTGAGC 255
QY 244 TCTGTGACTCGCGGACACGGCCGCTCTATTACTGTGGCGGTGAGATGGGTATCTTTG 303
Db 256 TCTGTGACCGCGCGGACACGGCCGCTGTATTACTGTGCCAGAGGGGACTGGGGTACTTTT 315
QY 304 GACAACTGGGGCCAGGGAACCCCTGGTCACCGTCTC 338
Db 316 GACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTC 350

RESULT 11
US-10-613-27
; Sequence 27, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; PRIOR FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-613-27
```

```
Query Match 76.1%; Score 260.4; DB 15; Length 358;
Best Local Similarity 87.1%; Pred. No. 9.5e-77;
Matches 298; Conservative 0; Mismatches 41; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCCGACGACTGGTGAAGCCTTTCACAGACCCCTGTCCCTCACCTGCACCTGTCTCT 63
Db 16 GAGTCGGGCCCGACGACTGGTGAAGCCTTTCACAGACCCCTGTCCCTCACCTGCACCTGTCTCT 75
QY 64 GGTGGCTCCATCCGACGTGGTGTATTATTGGAGTTGGTCCGCCAGCCTCCAGGGAAG 123
Db 76 GGTGGCTCCATCCGACGTGGTGTATTACTTGGAGCTGGATCCGCCAGCCTCCAGGGAAG 135
QY 124 GGCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTTCAACAACCCCGTCCCTC 183
Db 136 GGCTGGAGTGGATGGGTACATCTATTCAGTGGGAGCCTACTACAAACCCGTCCTC 195
QY 184 AAGAGTCGAATTACCATGTCTAGTAGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 243
Db 196 AAGAGTCGAATTACCTATCAGTAGACACGCTTAAGAACCACTTCTCCCTGAAGCTGAAC 255
QY 244 TCTGTGACTCGCGGACACGGCCGCTCTATTACTGTGGCGG---GTGAGATGGGTACT 300
Db 256 TCTATGACTCGCGGACACGGCCGCTGTATTACTGTGGGAGATCGGGAAACACAGCTGGT 315
QY 301 TTGGACACTGGGGCCAGGGAACCCCTGGTCACCGTCTCTCA 342
Db 316 TTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCTCA 357
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```
RESULT 12
US-10-530-530-27
```

```
; Sequence 27, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-530-27
```

```
Query Match 76.1%; Score 260.4; DB 15; Length 358;
Best Local Similarity 87.1%; Pred. No. 9.5e-77;
Matches 298; Conservative 0; Mismatches 41; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCCGACGACTGGTGAAGCCTTTCACAGACCCCTGTCCCTCACCTGCACCTGTCTCT 63
Db 16 GAGTCGGGCCCGACGACTGGTGAAGCCTTTCACAGACCCCTGTCCCTCACCTGCACCTGTCTCT 75
QY 64 GGTGGCTCCATCCGACGTGGTGTATTATTGGAGTTGGTCCGCCAGCCTCCAGGGAAG 123
Db 76 GGTGGCTCCATCCGACGTGGTGTATTACTTGGAGCTGGATCCGCCAGCCTCCAGGGAAG 135
QY 124 GGCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTTCAACAACCCCGTCCCTC 183
Db 136 GGCTGGAGTGGATGGGTACATCTATTCAGTGGGAGCCTACTACAAACCCGTCCTC 195
QY 184 AAGAGTCGAATTACCATGTCTAGTAGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 243
Db 196 AAGAGTCGAATTACCTATCAGTAGACACGCTTAAGAACCACTTCTCCCTGAAGCTGAAC 255
QY 244 TCTGTGACTCGCGGACACGGCCGCTCTATTACTGTGGCGG---GTGAGATGGGTACT 300
Db 256 TCTATGACTCGCGGACACGGCCGCTGTATTACTGTGGGAGATCGGGAAACACAGCTGGT 315
QY 301 TTGGACACTGGGGCCAGGGAACCCCTGGTCACCGTCTCTCA 342
Db 316 TTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCTCA 357
```

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RESULT 13
US-10-357-27
; Sequence 27, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-660-357-27
```

```
Query Match 76.1%; Score 260.4; DB 17; Length 358;
Best Local Similarity 87.1%; Pred. No. 9.5e-77;
Matches 298; Conservative 0; Mismatches 41; Indels 3; Gaps 1;
```

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTACAGACCCCTGTCCCTCACCTGCACTGTCTCT 63
Db 16 GAGTGGGGCCAGGACTGGTGAAGCCTTACAGACCCCTGTCCCTCACCTGCACTGTCTCT 75
QY 64 GGTGGCTCCATCCGAGTGGTGGTTATTATTGGAGTTGGGTCCGCGAGCCTCCAGGGAAG 123
Db 76 GGTGGCTCCATCAACAGTGGTGGTTACTGCTACTGGAGCTGGATCCGCGAGCACCAGGGAAG 135
QY 124 GGCCTGGAGTGGATCGGCAACATCTATCAGCTGGGCAACACCTTACAGACCCCTGTCCCTCACCTGCACTGTCTCT 183
Db 136 GGCCTGGAGTGGATCGGCAACATCTATCAGCTGGGCAACACCTTACAGACCCCTGTCCCTCACCTGCACTGTCTCT 195
QY 184 AAGAGTCGAATTACCTTATCAGTAGACAGCTCTAAGAACCTTCTCCCTGAGACTGACC 243
Db 196 AAGAGTCGAATTACCTTATCAGTAGACAGCTCTAAGAACCTTCTCCCTGAGACTGACC 255
QY 244 TCTGTGACTGCGCGGACACCGCGCTGTATTACTGTGCGCG---GTGAGATGGGTATCT 300
Db 256 TCTGTGACTGCGCGGACACCGCGCTGTATTACTGTGCGAGAGATCGGGAACAGCTGCT 315
QY 301 TTGGACAACCTGGGCGCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342
Db 316 TTGTGACTGGGCGCAGGGAACCCCTGGTCAACCGTCTCTCTCA 357

RESULT 14

US-10-309-762-186
; Sequence 186, Application US/10309762
; Publication No. US20040018198A1

; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean

; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa

; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXY ANHYDRASE IX

; FILE REFERENCE: (CA IX) TUMOR ANTIGEN
; CURRENT APPLICATION NUMBER: US/10/309,762

; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275

; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 186

; LENGTH: 370
; TYPE: DNA

; ORGANISM: Homo sapiens
US-10-309-762-186

Query Match 75.0%; Score 256.4; DB 16; Length 370;
Best Local Similarity 85.6%; Pred. No. 2.1e-75;

Matches 303; Conservative 0; Mismatches 36; Indels 15; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTACAGACCCCTGTCCCTCACCTGCACTGTCTCT 63
Db 16 GAGTGGGGCCAGGACTGGTGAAGCCTTACAGACCCCTGTCCCTCACCTGCACTGTCTCT 75
QY 64 GGTGGCTCCATCCGAGTGGTGGTTATTATTGGAGTTGGGTCCGCGAGCCTCCAGGGAAG 123
Db 76 GGTGGCTCCATCAGAGTGGTGGTTACTGCTGGAGCTGGATCCGCGAGCACCAGGGAAG 135
QY 124 GGCCTGGAGTGGATCGGCAACATCTATCAGCTGGGCAACACCTTACAGACCCCTGTCCCTCACCTGCACTGTCTCT 183
Db 136 GGCCTGGAGTGGATCGGCAACATCTATCAGCTGGGCAACACCTTACAGACCCCTGTCCCTCACCTGCACTGTCTCT 195
QY 184 AAGAGTCGAATTACCTTATCAGTAGACAGCTCTAAGAACCTTCTCCCTGAGACTGACC 243
Db 196 AAGAGTCGAATTACCTTATCAGTAGACAGCTCTAAGAACCTTCTCCCTGAGACTGACC 255
QY 244 TCTGTGACTGCGCGGACACCGCGCTGTATTACTGTGCGCGTCAAG----- 289
Db 256 TCTGTGACTGCGCGGACACCGCGCTGTATTACTGTGCGAGAGCGGGGAATATCTATGCT 315

QY 290 -ATGGGTATATTTGGACAACCTGGGCGCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342
Db 316 TCGGGAGGTTACTTGGACTACTGGGCGCAGGGAACCCCTGGTCAACCGTCTCTCTCA 369

RESULT 15

US-10-309-762-110

; Sequence 110, Application US/10309762
; Publication No. US20040018198A1

; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean

; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa

; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXY ANHYDRASE IX

; FILE REFERENCE: (CA IX) TUMOR ANTIGEN
; CURRENT APPLICATION NUMBER: US/10/309,762

; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275

; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110

; LENGTH: 429
; TYPE: DNA

; ORGANISM: Homo sapiens
US-10-309-762-110

Query Match 74.6%; Score 255; DB 16; Length 429;
Best Local Similarity 85.2%; Pred. No. 6.5e-75;

Matches 304; Conservative 0; Mismatches 35; Indels 18; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTACAGACCCCTGTCCCTCACCTGCACTGTCTCT 63
Db 73 GAGTGGGGCCAGGACTGGTGAAGCCTTACAGACCCCTGTCCCTCACCTGCACTGTCTCT 132
QY 64 GGTGGCTCCATCCGAGTGGTGGTTATTATTGGAGTTGGGTCCGCGAGCCTCCAGGGAAG 123
Db 133 GGTGGCTCCATCAGAGTGGTGGTTACTGCTGGAGCTGGATCCGCGAGCACCAGGGAAG 192
QY 124 GGCCTGGAGTGGATCGGCAACATCTATCAGCTGGGCAACACCTTACAGACCCCTGTCCCTCACCTGCACTGTCTCT 183
Db 193 GGCCTGGAGTGGATCGGCAACATCTATCAGCTGGGCAACACCTTACAGACCCCTGTCCCTCACCTGCACTGTCTCT 252
QY 184 AAGAGTCGAATTACCTTATCAGTAGACAGCTCTAAGAACCTTCTCCCTGAGACTGACC 243
Db 253 AAGAGTCGAATTACCTTATCAGTAGACAGCTCTAAGAACCTTCTCCCTGAGACTGACC 312
QY 244 TCTGTGACTGCGCGGACACCGCGCTGTATTACTGTGCGCGTCAAGATGGGTATCTTTG 303
Db 313 TCTGTGACTGCGCGGACACCGCGCTGTATTACTGTGCGAGAGAAATTACGATATTTG 372
QY 304 -----GACAATGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342
Db 373 ACTGGTTTCAACTGGTTCGACCCCTGGGCGCAGGGAACCCCTGGTCAACCGTCTCTCTCA 429

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Job time : 761.173 secs

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OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 00:21:37 ; Search time 48.3636 Seconds

(without alignments)
3924.296 Million cell updates/sec

Title: US-10-027-725A-2

Perfect score: 342

Sequence: 1 ctgagctcgtgccaggact.....ccctggtcacctctctctca 342

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

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- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	251.2	73.5	516	4	US-09-472-087-33
2	249.2	72.9	357	1	US-08-360-125-3
3	249.2	72.9	357	2	US-08-450-578-3
4	249.2	72.9	357	2	US-09-017-628-3
5	249.2	72.9	357	2	US-09-014-880-3
6	249.2	72.9	357	4	US-08-450-363-3
7	243	71.1	450	4	US-09-582-337-13
8	242.6	70.9	631	3	US-08-545-809A-31
9	237.4	69.4	1567	3	US-09-049-672A-17
10	234.6	68.6	1543	4	US-09-800-729-74
11	230.6	67.4	366	1	US-08-360-125-9
12	230.6	67.4	366	2	US-08-450-578-9
13	230.6	67.4	366	2	US-09-017-628-9
14	230.6	67.4	366	2	US-09-014-880-9
15	230.6	67.4	366	4	US-08-450-363-9
16	225	65.8	1212	3	US-08-545-809A-61
17	223.4	65.3	800	3	US-08-545-809A-39
18	215.6	63.0	750	4	US-10-039-785-62
19	215.2	62.9	403	3	US-09-042-353-357
20	215.2	62.9	403	4	US-08-758-417A-205
21	215	62.9	840	3	US-09-260-527-4
22	212	62.0	524	3	US-09-042-353-419
23	212	62.0	524	4	US-08-758-417A-219
24	212	62.0	4926	3	US-09-042-353-418
25	212	62.0	4926	4	US-08-758-417A-268
26	210.6	61.6	732	4	US-10-039-785-56
27	208	60.8	288	3	US-08-851-362D-7

Sequence 355, App
Sequence 203, App
Sequence 55, Appl
Sequence 45, Appl
Sequence 11, Appl
Sequence 20, Appl
Sequence 23, Appl
Sequence 28, Appl
Sequence 3, Appl
Sequence 7, Appl
Sequence 59, Appl
Sequence 3, Appl
Sequence 4, Appl
Sequence 9, Appl
Sequence 5, Appl
Sequence 7, Appl
Sequence 9, Appl

US-09-042-353-355
US-08-758-417A-203
US-08-545-809A-55
US-08-477-553A-45
US-08-851-362D-11
US-08-652-816A-20
US-08-652-816A-23
US-08-545-809A-28
US-08-793-450-3
US-08-793-450-7
US-08-545-809A-59
US-08-851-362D-3
US-08-545-809A-4
US-08-851-362D-9
US-08-259-372A-5
US-08-468-671-5
US-08-523-894-7
US-08-523-894-9

ALIGNMENTS

RESULT 1

US-09-472-087-33

; Sequence 33, Application US/09472087

; Patent No. 6682736

; GENERAL INFORMATION:

; APPLICANT: HANSON, DOUGLAS C.

; APPLICANT: NEVEU, MARK J.

; APPLICANT: MUELLER, ELLEN E.

; APPLICANT: HANKE, JEFFREY H.

; APPLICANT: GILMAN, STEVEN C.

; APPLICANT: DAVIS, C. GEOFFREY

; APPLICANT: CORVALAN, JOSE R.

; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4

; FILE REFERENCE: ABX-PF1

; CURRENT APPLICATION NUMBER: US/09/472,087

; CURRENT FILING DATE: 1999-12-23

; PRIOR APPLICATION NUMBER: 60/113,647

; PRIOR FILING DATE: 1998-12-23

; NUMBER OF SEQ ID NOS: 147

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 33

; LENGTH: 516

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-472-087-33

Query Match 73.5%; Score 251.2; DB 4; Length 516;

Best Local Similarity 85.7%; Pred. No. 1.1e-68;

Matches 293; Conservative 0; Mismatches 43; Indels 6; Gaps 1;

Qy	7	TCGTGCCAGGACTGGTGAAGCCCTTACAGACCCCTGTCCTTCCCTCAGCTGTCTCTGGT	66
Db	1	TCGGGCCAGGACTGGTGAAGCCCTTACAGATCTGTCTCTCCTCAGCTGTCTCTGGT	60
Qy	67	GGCTCCATCCGAGTGGTGTATATTGGAGTGGTCCGCCAGCTCCAGGGAAGGGC	126
Db	61	GGCTCCATCAGCAGTGGTGGTCTACTTGGAGCTGGATCCGCCAGCACCCAGGGAAGGGC	120
Qy	127	CTGGAGTGGATCCGCACATCTATCATCAGTGGGGAACACCTTACACACCCGTCCTCAAG	186
Db	121	CTGGAGTGGATGGGTGATCTATTATCTGGGGAACACCTTACACACCCGTCCTCAAG	180
Qy	187	AGTCGAATTACCATGTGAGTAGACACCTTAAAGAACCATTTCTCCCTGAGACTGACCTCT	246
Db	181	AGTCGAATTACCATGTGAGTAGACACCTTAAAGAACCATTTCTCCCTGAGACTGAGCTCT	240
Qy	247	GTGACTCCGCGGACACGGCCGCTATTATGTGCGCGGTCCAGATGGG-----TATACT	300
Db	241	GTGACTCCGCGGACACGGCCGCTATTATTTGTGCGGAGATAGTGGGGACTACTACGGT	300

MEDIUM TYPE: Diskette, 5.25 inch, 500 kb.

COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,578

FILING DATE: May 25, 1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/360,125

FILING DATE: December 20, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/905,534

FILING DATE: June 29, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.

REGISTRATION NUMBER: 33,367

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-8850

TELEFAX:

TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 357 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cdNA

HYPOTHETICAL:

ANTI-SENSE:

FRAGMENT TYPE:

ORIGINAL SOURCE:

ORGANISM:

STRAIN:

INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:

HAPLOTYPE:

TISSUE TYPE:

CELL TYPE: Hybridoma producing human

CELL TYPE: antibody GAH

CELL LINE:

ORGANELLE:

IMMEDIATE SOURCE:

LIBRARY:

CLONE:

POSITION IN GENOME:

CHROMOSOME/SEGMENT:

MAP POSITION:

UNITS:

FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION:

PUBLICATION INFORMATION:

AUTHORS:

TITLE:

JOURNAL:

VOLUME:

PAGES:

DATE:

DOCUMENT NUMBER:

FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-08-450-578-3

Query Match 72.9%; Score 249.2; DB 2; Length 357;

Best Local Similarity 85.1%; Pred. No. 4e-68;

Matches 291; Conservative 0; Mismatches 48; Indels 3; Gaps 1;

US-08-450-578-3

QY 4 GAGTCTGGCCCGAGGACTGGTGAAGCCTTCACAGACCTGTCCTCCTCAGCTGCTCTCT 63
DB 16 GAGTCGGGCCCGAGGACTGGTGAAGCCTTCACAGACCTGTCCTCCTCAGCTGCTCTCT 75
QY 64 GGTGGCTCCATCCGAGTGGTGGTTATTATTTGAGTGGGTCCGCGAGCCTCCAGGAAG 123
DB 76 GGTGGCTCCATCAGCAGTGGTGGTTTCTTACTGGAAGTGGATCCGCGAGCACCAGGAAG 135
QY 124 GGCTGGAGTGGATCGGCAACATCTATCAGTGGGCAACACCTTACACACCCGTCCTC 183
DB 136 GGCTGGAGTGGATCGGTCATCTATTACAGTGGGAGCACCCTACTACACCCGTCCTC 195
QY 184 AAGAGTCGAATTACCATGTCTAGTACAGTCTTAAGAACCTTCTCCCTGAGACTGACC 243
DB 196 AAGAGTCGAGTTACCATATCGTAGACAGTCTTAAGAGCAGTCTCCCTGAGACTGAGC 255
QY 244 TCTGTGACTGCCGCGACACGGCCGCTATTACTGTGCGGGTTCAGATGGGTATATTG 303
DB 256 TCTGTGACTGCCGCGACACGGCCGCTATTACTGTGCGAGGTCTACCCGACTACGGGG 315
QY 304 ---GACAACTGGGGCCAGGGAACCCCTGTCACCGTCTCTCA 342
DB 316 GCTGACTACTGGGGCCAGGGAACATGGTCACCGTCTCTTCA 357

RESULT 4

US-09-017-628-3

; Sequence 3, Application US/09017628

; Patent No. 5990287

; GENERAL INFORMATION:

; APPLICANT: HOSOKAWA, Saiko

; APPLICANT: TAGAWA, Toshiaki

; APPLICANT: HIRAKAWA, Yoko

; APPLICANT: ITO, No. 5990287hiko

; APPLICANT: NAGAIKE, Kazuhiro

; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO

; TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE

; FILE REFERENCE: 177/527361KH

; CURRENT APPLICATION NUMBER: US/09/017,628

; CURRENT FILING DATE: 1998-02-02

; EARLIER APPLICATION NUMBER: 08/360,125

; EARLIER FILING DATE: 1994-12-20

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 357

; TYPE: DNA

; ORGANISM: Unknown

; FEATURE:

; OTHER INFORMATION: Hybridoma producing human antibody GAH

US-09-017-628-3

Query Match 72.9%; Score 249.2; DB 2; Length 357;

Best Local Similarity 85.1%; Pred. No. 4e-68;

Matches 291; Conservative 0; Mismatches 48; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCCGAGGACTGGTGAAGCCTTCACAGACCTGTCCTCCTCAGCTGCTCTCT 63
DB 16 GAGTCGGGCCCGAGGACTGGTGAAGCCTTCACAGACCTGTCCTCCTCAGCTGCTCTCT 75
QY 64 GGTGGCTCCATCCGAGTGGTGGTTATTATTTGAGTGGGTCCGCGAGCCTCCAGGAAG 123
DB 76 GGTGGCTCCATCAGCAGTGGTGGTTTCTTACTGGAATGGATCCGCGAGCACCAGGAAG 135
QY 124 GGCTGGAGTGGATCGGCAACATCTATCAGTGGGCAACACCTTACAAACCCGTCCTC 183
DB 136 GGCTGGAGTGGATGGGTACATCTATTACAGTGGGAGCACCTACTACTACACCCGTCCTC 195
QY 184 AAGAGTCGAATTACCATGTCTAGTACAGCCTTAAGAACCTTCTCCCTGAGACTGACC 243
DB 196 AAGAGTCGAGTTACCATATCGTAGACAGTCTTAAGAGCCAGTCTCCCTGAAGCTGAGC 255
QY 244 TCTGTGACTGCCGCGACACGGCCGCTATTACTGTGCGGGTTCAGATGGGTATATTG 303

Db 256 TCTCTGACTGCGCGGACACGCGCGTGTATTACTGTGGAGGTCTACCGGACTACGGGGG 315
QY 304 ---GACAAGTGGGGCCAGGACCTGTGTCACCGTCTCTCA 342
Db 316 GCTGACTACTGGGGCCAGGGAACAATGGTCAACCGTCTCTTCA 357

RESULT 5

US-09-014-880-3
; Sequence 3, Application US/09014880
; Patent No. 5990297
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA et al.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
; TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., #800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/014,880
; FILING DATE: January 28, 1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/450,578
; FILING DATE: May 25, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-721-8200
; TELEFAX: 202-721-8250
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; CELL TYPE: Hybridoma producing human
; CELL TYPE: antibody GAH

US-09-014-880-3

Query Match 72.9%; Score 249.2; DB 2; Length 357;
Best Local Similarity 85.1%; Pred. No. 4e-68;
Matches 291; Conservative 0; Mismatches 48; Indels 3; Gaps 1;
QY 4 GAGTCTGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACTGCACTGTCTCT 63
Db 16 GAGTGGGCGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACTGCACTGTCTCT 75
QY 64 GTGGCTCATCCGAGTGGTGGTTATTATTGGTTCGGTCCGCGCAGCCTCCAGGGGAG 123
Db 76 GTGGCTCATCAGCAGTGTGGTTTCTACTGGAACTGGATCCGCCAGCACCCAGGGGAG 135

QY 124 GSCCTGGAGTGATCGGCAACATCTATCAGTGGCAACACCTACAACACCGTCCCTC 183
Db 136 GSCCTGGAGTGATTTGGGTACATCTATTACAGTGGGAGCACCTACTACACCGTCCCTC 195
QY 184 AAGAGTCGAATTTACCATGTCTAGTAGACACAGTCTAAGAACCACCTTCTCCCTGAGACTGACC 243
Db 196 AAGAGTCGAGTTTACCATATCGTAGACACAGTCTAAGAGCCAGTTCTCTCCTGAAGCTGAGC 255
QY 244 TCTGTGACTGCGCGGACACGCGCGTCTATTACTGTGCGGCTCAGATGGGTATCTTTG 303
Db 256 TCTCTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGGTCTACCCGACTACGGGGG 315
QY 304 ---GACAACTGGGGCCAGGGAACCTGTGTCACCGTCTCTCTCA 342
Db 316 GCTGACTACTGGGGCCAGGGAACAATGGTCAACCGTCTCTTCA 357

RESULT 6

US-08-450-363-3
; Sequence 3, Application US/08450363
; Patent No. 6436434
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 6436434ihiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,363
; FILING DATE: May 25, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:

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; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human
; CELL TYPE: antibody GAH
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
; US-08-450-363-3

Query Match
Best Local Similarity 72.9%; Score 249.2; DB 4; Length 357;
Matches 291; Conservative 0; Mismatches 48; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCAGCTGCTCT 63
Db 16 GAGTGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCAGCTGCTCT 75
QY 64 GGTGGCTCCATCGCAGTGGTGTATTATTTGAGTTGGTGGCAGACCTCCAGGGAAG 123
Db 76 GGTGGCTCCATCGCAGTGGTGTATTATTTGAGTTGGTGGCAGACCTCCAGGGAAG 135
QY 124 GGCTGGAGTGGATCGGCAACATCTATCAGTGGCAACACCTACAAACCCGTCCTC 183
Db 136 GGCTGGAGTGGATCGGCAACATCTATCAGTGGCAACACCTACAAACCCGTCCTC 195
QY 184 AAGAGTCGAATTACCATGTGAGTACAGTCTTAAGAACCACTTCTCCCTGAGACTGACC 243
Db 196 AAGAGTCGAATTACCATGTGAGTACAGTCTTAAGAACCACTTCTCCCTGAGACTGACC 255
QY 244 TCTGTGACTCCCGGACACGCGCTCTATTACTGTCGGCGGTGAGTGGTACTTTG 303
Db 256 TCTGTGACTCCCGGACACGCGCTCTATTACTGTCGGCGGTGAGTGGTACTTTG 315
QY 304 ---GACAACTGGGCGCAGGGAACCCCTGGTCACCGTCTCTCTCA 342
Db 316 GCTGACTACTGGGCGCAGGGAACCAATGGTCACCGTCTCTCTCA 357

RESULT 7
US-09-582-337-13
; Sequence 13, Application US/09582337
; Patent No. 6562618
; GENERAL INFORMATION:
; APPLICANT: Japan Tobacco, Inc.
; TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
; TITLE OF INVENTION: and Medicinal Uses Thereof
```

```
; FILE REFERENCE: J1-009PCT
; CURRENT APPLICATION NUMBER: US/09/582,337
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: JP P1997-367699
; PRIOR FILING DATE: 1997-12-25
; PRIOR APPLICATION NUMBER: JP P1998-356183
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 13
; LENGTH: 450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(450)
; NAME/KEY: sig_peptide
; LOCATION: (1)..(58)
; NAME/KEY: V region
; LOCATION: (59)..(353)
; US-09-582-337-13

Query Match
Best Local Similarity 71.1%; Score 243; DB 4; Length 450;
Matches 303; Conservative 0; Mismatches 35; Indels 19; Gaps 2;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCAGCTGCTCTCT 63
Db 74 GAGTGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCAGCTGCTCTCT 132
QY 64 GGTGGCTCCATCGCAGTGGTGTATTATTTGAGTTGGTGGCAGACCTCCAGGGAAG 123
Db 133 GGTGGCTCCATCGCAGTGGTGTATTATTTGAGTTGGTGGCAGACCTCCAGGGAAG 192
QY 124 GGCTGGAGTGGATCGGCAACATCTATCAGTGGCAACACCTACAAACCCGTCCTC 183
Db 193 GGCTGGAGTGGATCGGCAACATCTATCAGTGGCAACACCTACAAACCCGTCCTC 252
QY 184 AAGAGTCGAATTACCATGTGAGTACAGTCTTAAGAACCACTTCTCCCTGAGACTGACC 243
Db 253 AAGAGTCGAATTACCATGTGAGTACAGTCTTAAGAACCACTTCTCCCTGAGACTGACC 312
QY 244 TCTGTGACTCCCGGACACGCGCTCTATTACTGTCGGCGGTGAGTGGTACTTTG 300
Db 313 TCTGTGACTCCCGGACACGCGCTCTATTACTGTCGGCGGTGAGTGGTACTTTG 372
QY 301 -----TTGGACAACTGGGCGCAGGGAACCCCTGGTCACCGTCTCTCTCA 342
Db 373 GGTATTACGACTACTTTGACTACTGGGCGCAGGGAACCCCTGGTCACCGTCTCTCTCA 429

RESULT 8
US-08-545-809A-31
; Sequence 31, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
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;; PRIOR APPLICATION NUMBER: 60/155,709
;; PRIOR FILING DATE: 1999-09-24
;; NUMBER OF SEQ ID NOS: 217
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 74
;; LENGTH: 1543
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-800-729-74

Query Match 68.6%; Score 234.6; DB 4; Length 1543;
Best Local Similarity 81.0%; Pred. No. 2.5e-63;
Matches 273; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 4 GAGTCTGGCCAGACAGTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGACCTGTCTCT 63
Db 90 GAGTCGGGCCAGACAGTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGACCTGTCTCT 149

Qy 64 GGTGGCTCCATCCGAGTGGTGGTTATTATTGGAGTTGGTCCGCCAGCCTCCAGGGAAG 123
Db 150 GTGGCTCCATCAGAGTGGTGGTCACTACTGGAGCTGGATCCGCCAGACCCAGGGAAG 209

Qy 124 GGCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACTACAAACCCCGTCCCTC 183
Db 210 GGCCTGGAGTGGATGGGTACATCTTTACAATGGGTCACTACTACAATCCGTCCCTC 269

Qy 184 AAGAGTCGAATTACATGTCTAGTACACAGCTCTAAGAACCACTTCTCCCTGAGACTGACC 243
Db 270 AAGAGTCGAGTTACCATATCTGTAGACACGCTCTCAGAACCACTTCTCCCTGAGCTGAGC 329

Qy 244 TCTGTGACTGCGCGGACACGGCGCTTATTACTGTGGCGGTGAGTGGGTATCTTTG 303
Db 330 TCTGTGACTGCGCGGACACGGCGCTTATTACTGTGGCGGAAGATCATCGAGGACACAGA 389

Qy 304 GACAACTGGGCCAGGGAACCTCGTCACCGTCTCTCT 340
Db 390 GACGGTACCAGCTGGAATACCGAGGCTTTGACTACT 426

RESULT 11
US-08-360-125-9
; Sequence 9, Application US/08360125
; Patent No. 5767246
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5767246ihiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,125
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; APPLICATION NUMBER:

;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warren M. Cheek, Jr.
;; REGISTRATION NUMBER: 33,367
;; REFERENCE/DOCKET NUMBER:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-8850
;; TELEFAX:
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 366 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: cdna
;; HYPOTHETICAL:
;; ANTI-SENSE:
;; FRAGMENT TYPE:
;; ORIGINAL SOURCE:
;; ORGANISM:
;; STRAIN:
;; INDIVIDUAL ISOLATE:
;; DEVELOPMENTAL STAGE:
;; HAPLOTYPE:
;; TISSUE TYPE:
;; CELL TYPE: Hybridoma producing human antibody 1-3-1
;; CELL LINE:
;; ORGANELLE:
;; IMMEDIATE SOURCE:
;; LIBRARY:
;; CLONE:
;; POSITION IN GENOME:
;; CHROMOSOME/SEGMENT:
;; MAP POSITION:
;; UNITS:
;; FEATURE:
;; NAME/KEY:
;; LOCATION:
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION:
;; PUBLICATION INFORMATION:
;; AUTHORS:
;; TITLE:
;; JOURNAL:
;; VOLUME:
;; ISSUE:
;; PAGES:
;; DATE:
;; DOCUMENT NUMBER:
;; FILING DATE:
;; PUBLICATION DATE:
;; RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-9

Query Match 67.4%; Score 230.6; DB 1; Length 366;
Best Local Similarity 81.2%; Pred. No. 2.4e-62;
Matches 285; Conservative 0; Mismatches 54; Indels 12; Gaps 1;

Qy 4 GAGTCTGGCCAGACAGTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGACCTGTCTCT 63
Db 16 GAGTCGGGCCAGACAGTGGTGAAGCCTTCGAGACCCCTGTCCTCACCTGACCTGTCTCT 75

Qy 64 GGTGGCTCCATCCGAGTGGTGGTTATTATTGGAGTTGGTCCGCCAGCCTCCAGGGAAG 123
Db 76 GGTGGCTCCATCAGCAGTAGTACTACTGGGGCTGGATCCGCCAGGCCCGCCAGGGAAG 135

Qy 124 GGCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACTACACACCCCGTCCCTC 183
Db 136 GGGCTGGAGTGGATGGGAGTATCTATTATAGTGGGAGCACCTACTACAACCCGTCCTC 195

Qy 184 AAGAGTCGAATTACCATGTCTAGTAGACACCTCTAAGAACCCACTTCTCCCTGAGACTGACC 243

Db 196 AAGATCGAGTCACCATATCCGTAGACACAGTCCAAAGAACAGTTCTCCCTGAAGCTGAGC 255
QY 244 TCTGTGACTGGCGGACACGGCGCTTATTACTGTGG-----CGGTGAGAT 291
Db 256 TCTGTGACCGCGGACACAGCGCTGTATTACTGTGGAGGGGAGCTACGGGGGCTAC 315
QY 292 GGGTATACCTTTGGCAAACTGGGGCCAGGGAACCTGGTCACCGTCTCCTCA 342
Db 316 TACTACGGTATGGACGCTGTGGGGCCAAAGGACCACGGTCACGCTCTCCTCA 366

RESULT 12

US-08-450-578-9
; Sequence 9, Application US/08450578
; Patent No. 5837845
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5837845ihiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,578
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 366 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human antibody 1-3-1

; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-578-9

Query Match 67.4%; Score 230.6; DB 2; Length 366;
Best Local Similarity 81.2%; Pred. No. 2.4e-62;
Matches 285; Conservative 0; Mismatches 54; Indels 12; Gaps 1;

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Db 76 GGTGGCTCCATCAGCAGTAGTAGTTACTACTGGGCTGGATCCGCGCAGCCCCCAGGGAAG 135
QY 124 GGCCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACCTTACAAACCCGTCCTC 183
Db 136 GGGCTGGAGTGGATGGGAGTATCTATTATAGTGGGAGCCTACTACAAACCCGTCCTC 195
QY 184 AAGAGTCGAATTACCATGTAGTAGACACAGTCTAAGAACCACTTCTCCCTGAGACTGACC 243
Db 196 AAGAGTCGAGTCACCATATCGTAGACACAGTCCAGAACCACTTCTCCCTGAGACTGACC 255
QY 244 TCTGTGACTGGCGGACACAGCGCGTCTATTACTGTGCG-----CGGTGAGAT 291
Db 256 TCTGTGACCGCGGACAGACAGCGTGTATTACTGTGCGAGGGGAGCTACGGGGGCTAC 315
QY 292 GGGTATACCTTTGGCAAACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA 342
Db 316 TACTACGGTATGGACGCTGTGGGGCCAAAGGACCACGGTCACGCTCTCCTCA 366

RESULT 13

US-09-017-628-9
; Sequence 9, Application US/09017628
; Patent No. 5990287
; GENERAL INFORMATION:
; APPLICANT: HOSOKAWA, Saiko
; APPLICANT: TAGAWA, Toshiaki
; APPLICANT: HIRAKAWA, Yoko
; APPLICANT: ITO, No. 5990287ihiko
; APPLICANT: NAGAIKE, Kazuhiro
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
; TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; FILE REFERENCE: 177/527361KH
; CURRENT APPLICATION NUMBER: US/09/017,628
; CURRENT FILING DATE: 1998-02-02
; EARLIER APPLICATION NUMBER: 08/360,125

EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 366
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Hybridoma producing human antibody 1-3-1
US-09-017-628-9

Query Match 67.4%; Score 230.6; DB 2; Length 366;
Best Local Similarity 81.2%; Pred. No. 2.4e-62;
Matches 285; Conservative 0; Mismatches 54; Indels 12; Gaps 1;

Qy 4 GAGTCTGCCCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACTGTCTCT 63
Db 16 GAGTCGGGCCAGGACTGGTGAAGCCTTCGAGAGCCCTGTCCTCACCTGCACTGTCTCT 75

Qy 64 GGTGGCTCCATCCGACGTGGTGTATATATGGAGTTGGTCCGCGAGCCTCCAGGGAAG 123
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Qy 124 GGCTCTGAGTGGATCGGCAACATCTATCAGAGTGGCAACACCTACCAACACCCGTCCTC 183
Db 136 GGGCTGGAGTGGATGGAGTAUATCTATATAGTGGAGCACCTACTAACAACCCGTCCTC 195

Qy 184 AAGAGTCGAATTACCATGTCTAGTAGACACGCTCTAAGAACCACTTCTCCCTGAGACTGACC 243
Db 196 AAGAGTCGAGTCACCATCGTAGACAGCTGCCAAGAACGAGTCTCCCTGAAGCTGAGC 255

Qy 244 TCTGTGACTGCGCGGACACGGCCGTCTATTACTGTGG-----CGTTCAGAT 291
Db 256 TCTGTGACCGCGGACACGGCCGTCTATTACTGTGCGAGGGGAGCTACGGGGGGTAC 315

Qy 292 GGGTATCTTTGGACAATGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342
Db 316 TACTACGTATGGAGCTGTGGGGCCAGGGACCAACGCTACCGTCTCTCTCA 366

RESULT 14
US-09-014-880-9
Sequence 9, Application US/09014880
Patent No. 5990297
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA et al.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,880
FILING DATE: January 28, 1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/450,578
FILING DATE: May 25, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534

FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
US-09-014-880-9

Query Match 67.4%; Score 230.6; DB 2; Length 366;
Best Local Similarity 81.2%; Pred. No. 2.4e-62;
Matches 285; Conservative 0; Mismatches 54; Indels 12; Gaps 1;

Qy 4 GAGTCTGCCCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACTGTCTCT 63
Db 16 GAGTCGGGCCAGGACTGGTGAAGCCTTCGAGAGCCCTGTCCTCACCTGCACTGTCTCT 75

Qy 64 GGTGGCTCCATCCGACGTGGTGTATATATGGAGTTGGTCCGCGAGCCTCCAGGGAAG 123
Db 76 GGTGGCTCCATCCGACGTGGTGTATATATGGAGTTGGTCCGCGAGCCTCCAGGGAAG 135

Qy 124 GGCTCTGAGTGGATCGGCAACATCTATCAGAGTGGCAACACCTACTAACAACCCGTCCTC 183
Db 136 GGGCTGGAGTGGATGGAGTAUATCTATATAGTGGAGCACCTACTAACAACCCGTCCTC 195

Qy 184 AAGAGTCGAATTACCATGTCTAGTAGACACGCTCTAAGAACCACTTCTCCCTGAGACTGACC 243
Db 196 AAGAGTCGAGTCACCATCGTAGACAGCTGCCAAGAACGAGTCTCCCTGAAGCTGAGC 255

Qy 244 TCTGTGACTGCGCGGACACGGCCGTCTATTACTGTGG-----CGTTCAGAT 291
Db 256 TCTGTGACCGCGGACACGGCCGTCTATTACTGTGCGAGGGGAGCTACGGGGGGTAC 315

Qy 292 GGGTATCTTTGGACAATGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342
Db 316 TACTACGTATGGAGCTGTGGGGCCAGGGACCAACGCTACCGTCTCTCTCA 366

RESULT 15
US-08-450-363-9
Sequence 9, Application US/08450363
Patent No. 6436434
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 6436434/hiho ITO
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,363
FILING DATE: May 25, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:

Query Match 67.4%; Score 230.6; DB 4; Length 366;
Best Local Similarity 81.2%; Pred. No. 2.4e-62;
Matches 285; Conservative 54; Mismatches 54; Indels 12; Gaps 1;
US-08-450-363-9
QY 4 GAGTCGCGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACCTGCTCT 63
DB 16 GAGTCGCGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACCTGCTCT 75

QY 64 GGTGGCTCCATCCGCAAGTGGTGGTTATTATTGGAGTTGGGTCGCGCAGCTCCAGGGAAG 123
DB 76 GGTGGCTCCATCCGCAAGTGGTGGTTATTATTGGAGTTGGGTCGCGCAGCTCCAGGGAAG 135
QY 124 GGCCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTACAAACACCCGTCCTC 183
DB 136 GGGCTGGAGTGGATTGGGAGTATCTATTATAGTGGGAGCACCTACTACAACCCGTCCTC 195
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DB 196 AAGAGTCGAGTCACCATATCCGTAGACACGTCCTCAAGAACCACTTCTCCCTGAGACTGACC 255
QY 244 TCTGTGACTGCGCGGACACGCGCTCTATTACTGTGCG-----CGGTCAAGAT 291
DB 256 TCTGTGACCGCGGACACGCGCTGTGTATTACTGTGCGGGGAGGCTACGGGGGCTAC 315
QY 292 GGGTATACCTTTGGACAACCTGGGGCCAGGGAACCCCTGGTCACCGTCTCTCTCA 342
DB 316 TACTACGGTATGGACGCTCTGGGGCCAGGGAACCGGTACCGGTCTCTCTCA 366

Search completed: August 13, 2004, 07:18:07
Job time : 49.3636 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 12, 2004, 19:27:23 ; Search time 1471.46 Seconds
(without alignments)
10073.859 Million cell updates/sec

Title: US-10-027-725A-3
Perfect score: 342
Sequence: 1 ctgagctctggccaggact.....ccctgggtcacggtctctca 342

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: gb_htg.*
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- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
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- 17: em_hum.*
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- 24: em_ph.*
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- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	338.8	99.1	342	9	HSA458384 Homo sapi
2	332.8	94.4	342	9	HSA458383 Homo sapi
3	308.4	90.2	342	9	HSA458382 Homo sapi
4	284.6	83.2	414	9	AF062112 Homo sapi
5	284.4	83.2	351	9	HSA244930 Homo sapi
6	284.4	83.2	360	6	AX061463 Sequence
7	283.6	82.9	411	9	HST22X1
8	283	82.7	354	9	HSA245064
9	283	82.7	360	9	HSU80129 Human immu
10	283	82.7	360	9	HSU80130 Human immu
11	282.8	82.7	358	9	AF021954 Homo sapi
12	281.8	82.4	403	12	AF452917 Synthetic
13	281.4	82.3	351	9	HSA245020 Homo sapi
14	280.2	81.9	414	9	HST14X13
15	280.2	81.9	414	9	HST14X4
16	280	81.9	363	9	HSU80131 Human immu
17	279.8	81.8	432	9	HSA491911 Homo sapi
18	278.4	81.4	357	9	HSA244949 Homo sapi
19	278.2	81.3	432	9	HSA491912 Homo sapi
20	277.2	81.1	354	9	HSA244955 Homo sapi
21	276.4	80.8	357	9	HSA279523 Homo sapi
22	276.2	80.8	362	9	HSU80166 Human immu
23	275.8	80.6	412	12	AF452912 Synthetic
24	275.6	80.6	417	9	HST14X9
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26	275	80.4	406	12	AF453047 Synthetic
27	274.8	80.4	357	9	HSA279541 Homo sapi
28	274.8	80.4	357	9	HSU80168 Human immu
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33	271.8	79.5	351	9	HSA244953 Homo sapi
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37	271.6	79.4	357	9	HSA279530 Homo sapi
38	271.6	79.4	357	9	HSA279538 Homo sapi
39	271.4	79.4	362	9	HSU80169 Human immu
40	271	79.2	360	9	AB067300 Homo sapi
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42	270.6	79.1	366	9	HSU80111 Human immu
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45	269.2	78.7	361	9	HSA279518 Homo sapi

ALIGNMENTS

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LOCUS HSA458384 342 bp mRNA linear PRI 30-APR-2002
DEFINITION Homo sapiens partial mRNA for immunoglobulin heavy chain variable region (IGHV gene), clone 100.
ACCESSION AJ458384
VERSION AJ458384.1 GI:20387067
KEYWORDS IGHV gene; immunoglobulin heavy chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Flicker,S., Steinberger,P., Norderhaug,L., Sperr,W.R., Majlesi,Y., Valent,P., Kraft,D. and Valenta,R.

TITLE Conversion of grass allergen-specific human IgE into a protective
IgG1 antibody
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 342)
AUTHORS Flicker,S.
TITLE Direct Submission
JOURNAL Submitted (24-APR-2002) Flicker S., Department of Pathophysiology,
General Hospital of Vienna, 3Q, Waehringer Guertel 18-20, A-1090
Vienna, AUSTRIA

FEATURES

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Best Local Similarity 99.4%; Pred. No. 2.7e-86; Indels 0; Gaps 0;

Matches 340; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 301 TTGGACAACTGGGGCCAGGAAACCTGGTCACCGTCTCTCTCA 342
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RESULT 2

HSA458383

LOCUS

DEFINITION

region (IGHV gene), clone 60.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

HSA458383 342 bp mRNA linear PRI 30-APR-2002

Homo sapiens partial mRNA for immunoglobulin heavy chain variable

region (IGHV gene), clone 60.

AJ458383

AJ458383.1 GI:20387065

IGHV gene; immunoglobulin heavy chain; variable region.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

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AUTHORS

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JOURNAL

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AUTHORS

TITLE

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 Flicker,S., Steinberger,P., Norderhaug,L., Sperr,W.R., Majlesi,Y.,

Valent,P., Kraft,D. and Valenta,R.

Conversion of grass allergen-specific human IgE into a protective

IgG1 antibody

Unpublished

2 (bases 1 to 342)

Flicker,S.

Direct Submission

Submitted (24-APR-2002) Flicker S., Department of Pathophysiology,

General Hospital of Vienna, 3Q, Waehringer Guertel 18-20, A-1090

Vienna, AUSTRIA

Location/Qualifiers

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/mol_type="mRNA"

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Query Match 94.4%; Score 322.8; DB 9; Length 342;

Best Local Similarity 96.5%; Pred. No. 1.1e-81;

Matches 330; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 CTCGAGTCGGCCAGGACTGGTGAAGCCTTCACAGACCTGTCCTCCCTACCTGCACTGTC 60

Db 1 CTCGAGTCGGCCAGGACTGGTGAAGCCTTCACAGACCTGTCCTCCCTACCTGCACTGTC 60

QY 61 TCTGTGGTCCATCCGACGAGTGGTATTACTGGAGTTGGATCGCCAGCGTCCAGGG 120

Db 61 TCTGTGGTCCATCCGACGAGTGGTATTACTGGAGTTGGATCGCCAGCGTCCAGGG 120

QY 121 AAGGCCCTGAGTCGAGTACATCTATCAGTGGCAACACCTACCAACCCGCTCC 180

Db 121 AAGGCCCTGAGTCGAGTACATCTATCAGTGGCAACACCTACCAACCCGCTCC 180

QY 181 CTCAGAGTCGAGTTACCATGTCAGTAGACAGTCTAAGAACCACTTCTCCCTGAGGCTG 240

Db 181 CTCAGAGTCGAGTTACCATGTCAGTAGACAGTCTAAGAACCACTTCTCCCTGAGGCTG 240

QY 241 AGCTCTGACTGCGCGGACACGGCCGCTGTTACTGTGCGAGGTCAGATGGGTACACT 300

Db 241 AGCTCTGACTGCGCGGACACGGCCGCTGTTACTGTGCGAGGTCAGATGGGTACACT 300

QY 301 TTGGACAACTGGGGCCAGGAAACCTGGTCACCGTCTCTCTCA 342

Db 301 TTGGACAACTGGGGCCAGGAAACCTGGTCACCGTCTCTCTCA 342

RESULT 3

HSA458382

LOCUS

DEFINITION

region (IGHV gene), clone 94.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

HSA458382 342 bp mRNA linear PRI 30-APR-2002

Homo sapiens partial mRNA for immunoglobulin heavy chain variable

region (IGHV gene), clone 94.

AJ458382

AJ458382.1 GI:20387063

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

KEYWORDS IGHV gene; immunoglobulin heavy chain; variable region.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Flicker, S., Steinberger, P., Norderhaug, L., Sperr, W.R., Majlesi, Y.,
 Valent, P., Kraft, D. and Valenta, R.
 TITLE Conversion of grass allergen-specific human IgE into a protective
 IgG1 antibody
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 342)
 AUTHORS Flicker, S.
 TITLE Direct Submission
 JOURNAL Submitted (24-APR-2002) Flicker S., Department of Pathophysiology,
 General Hospital of Vienna, 30, Waehringer Guertel 18-20, A-1090
 Vienna, AUSTRIA
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 QY 1 CTGAGTCTGCCCGAGACTGGTGAAGCTTACAGACCCCTGTCCTCACTGCTC 60
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 QY 61 TCTGGTCTCCATCCGAGTGGTGTATTACTGGAGTTGGATCCGCGAGCTCAGG 120
 DB |||||
 61 TCTGGCGCTCCATCCGAGTGGTGTATTACTGGAGTTGGATCCGCGAGCTCAGG 120
 QY 121 AAGGCGCTGGAGTGGATCGGGTACATCTATCACAGTGGCAACACTACAACCCGCTC 180
 DB |||||
 121 AAGGCGCTGGAGTGGATCGGGTACATCTATCACAGTGGCAACACTACAACCCGCTC 180
 QY 181 CTCAAGAGTCAGTTACATGTACGTAGACAGCTTAAAGAACCATTTCTCCCTGAGGCTG 240
 DB |||||
 181 CTCAAGAGTCGAATTGCGATGCGGTAGACAGCTCTGAGAACAAATTTCTCCCTGAGGCTG 240
 QY 241 AGCTCTGTGACTGCCGGGACAGCGCGTGTATTACTGTGGAGTTCAGATGGTACACT 300
 DB |||||
 241 AACTCTGTGACTGCCGGGACAGCGCGTGTATTACTGTGGAGTTCAGATGGTACACT 300
 QY 301 TTGACAACTGGGCGCAGGAACCCCTGGTCACCGTCTCCCTCA 342
 DB |||||
 301 TTGACAACTGGGCGCAGGAACCCCTGGTCACCGTCTCCCTCA 342

RESULT 4
 AF062112
 LOCUS AF062112 414 bp mRNA linear PRI 08-MAY-2001

DEFINITION Homo sapiens clone 2lu-26 immunoglobulin heavy chain variable
 region (IGH) mRNA, partial cds.
 ACCESSION AF062112
 VERSION AF062112.1 GI:3170686
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 414)
 AUTHORS Wang, X. and Stollar, B.D.
 TITLE Immunoglobulin VH gene expression in human aging
 JOURNAL Clin. Immunol. 93 (2), 132-142 (1999)
 MEDLINE 93459182
 PUBMED 10527689
 REFERENCE 2 (bases 1 to 414)
 AUTHORS Wang, X. and Stollar, B.D.
 TITLE Direct Submission
 JOURNAL Submitted (22-APR-1998) Biochemistry Department, Tufts University
 School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA
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 Matches 305; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 4 GAGTCTGGCCCGAGACTGGTGAAGCCCTTACAGACCCCTGTCCTCACTGCTCTCT 63
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 73 GAGTGGGCCCGAGACTGGTGAAGCCCTTACAGACCCCTGTCCTCACTGCTCTCT 132
 QY 64 GTGGCTTCCATCCGAGTGGTGTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 123
 DB |||||
 133 GTGGCTTCCATCAGCAGTGGTGATTACTACTGGAGTTGGATCCGCCAGCGGGAAG 192
 QY 124 GGCCTGGAGTGGATCGGTACATCTATCACAGTGGCAACACTTCCCTAGAGCTGAGC 183
 DB |||||
 193 GGCCTGGAGTGGATCGGTACATCTATCACAGTGGGAGCACCTACTACACCCGTCCTC 252
 QY 184 AAGAGTCGAGTTACCATGTCTAGTAGACAGTCTAAGAACCATTTCTCCCTGAGCTGAGC 243
 DB |||||
 253 AAGAGTCGAGTTACCATGTCTAGTAGACAGTCTAAGAACCATTTCTCCCTGAGCTGAGC 312
 QY 244 TCTGTGACTGCCCGGACACGCGCGTGTATTACTGTGGAGGTCAGATGGGTACATTG 303
 DB |||||
 313 TCTGTGACTGCCCGGACACGCGCGTGTATTACTGTGGCGGTGGTACCAGCAGCTGCTTT 372
 QY 304 GACAACTGGGGCCAGGGAACCCCTGGTCACCGTCTCTCTCA 342

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Db 373 GACTACTGGGCCAGGACCCCTGTCACCGTCTCTCTCA 411
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HSA244930 351 bp mRNA linear PRI 01-JUN-2000
LOCUS Homo sapiens mRNA for immunoglobulin mu heavy chain variable
DEFINITION region, partial, clone 1-A34.
ACCESSION AJ244930
VERSION AJ244930.1 GI:4995319
KEYWORDS Igm; Igm heavy chain; immunoglobulin mu heavy chain; variable
region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Dono, M., Zupo, S., Leanza, N., Melioli, G., Fogli, M., Melagrana, A.,
Chiorazzi, N. and Ferrarini, M.
TITLE Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic
marginal zone equivalents
JOURNAL J. Immunol. 164 (11), 5596-5604 (2000)
MEDLINE 20281644
PUBMED 10820234
REFERENCE 2 (bases 1 to 351)
AUTHORS Dono, M.
TITLE Direct Submission
JOURNAL Submitted (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca
sul Cancro, Immunologia Clinica, L.go Rosanna Benzi 10- Genova,
ITALY
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Best Local Similarity 91.5%; Pred. No. 1.1e-70;
Matches 313; Conservative 0; Mismatches 26; Indels 3; Gaps 1;
QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACTGTCTCT 63
Db 10 GAGTCCGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACTGTCTCT 69
QY 64 GTGGGTCCATCCGACAGTGGTGGTTATTACTGGAGTTGGATCCGCCAGCGCTCCAGGGAAG 123
Db 70 GTGGGTCCATCAGCAGTGGTGGTTATTACTGGAGTTGGATCCGCCAGCGCTCCAGGGAAG 129
QY 124 GSCCTGGAGTACGGGTACATCTATCAGTGGCAACACCTACAGCAACCCGTCCTC 183
Db 130 GSCCTGGAGTACGGGTACATCTATCAGTGGCAACACCTACAGCAACCCGTCCTC 189
RESULT 5
HSA244930 351 bp mRNA linear PRI 01-JUN-2000
LOCUS Homo sapiens mRNA for immunoglobulin mu heavy chain variable
DEFINITION region, partial, clone 1-A34.
ACCESSION AJ244930
VERSION AJ244930.1 GI:4995319
KEYWORDS Igm; Igm heavy chain; immunoglobulin mu heavy chain; variable
region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Dono, M., Zupo, S., Leanza, N., Melioli, G., Fogli, M., Melagrana, A.,
Chiorazzi, N. and Ferrarini, M.
TITLE Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic
marginal zone equivalents
JOURNAL J. Immunol. 164 (11), 5596-5604 (2000)
MEDLINE 20281644
PUBMED 10820234
REFERENCE 2 (bases 1 to 351)
AUTHORS Dono, M.
TITLE Direct Submission
JOURNAL Submitted (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca
sul Cancro, Immunologia Clinica, L.go Rosanna Benzi 10- Genova,
ITALY
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Query Match 83.2%; Score 284.4; DB 9; Length 351;
Best Local Similarity 91.5%; Pred. No. 1.1e-70;
Matches 313; Conservative 0; Mismatches 26; Indels 3; Gaps 1;
QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACTGTCTCT 63
Db 10 GAGTCCGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACTGTCTCT 69
QY 64 GTGGGTCCATCCGACAGTGGTGGTTATTACTGGAGTTGGATCCGCCAGCGCTCCAGGGAAG 123
Db 70 GTGGGTCCATCAGCAGTGGTGGTTATTACTGGAGTTGGATCCGCCAGCGCTCCAGGGAAG 129
QY 124 GSCCTGGAGTACGGGTACATCTATCAGTGGCAACACCTACAGCAACCCGTCCTC 183
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QY 184 AAGAGTCGAGTTACCATGTCAGTAGACACAGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db 190 AAGAGTCGAGTTACCATATCAGTAGACACAGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 249
QY 244 TCTGTGACTGCGCGGACACCGCGGTGTATTACTGTGCGA---GGTCAGATGGGTACTACT 300
Db 250 TCTGTGACTGCGCGGACACCGCGGTGTATTACTGTGCGAGAGCAAGAGGACTTCTAC 309
QY 301 TTGGACAACTGGGCGGAGGAAACCTGGTCAACCGTCTCTCTCA 342
Db 310 TTTGACTACTGGGCGGAGGAAACCTGGTCAACCGTCTCTCTCA 351
RESULT 6
AX061463 360 bp DNA linear PAT 22-JAN-2001
LOCUS Sequence 32 from Patent WO0100678.
DEFINITION AX061463
ACCESSION AX061463
VERSION AX061463.1 GI:12406598
KEYWORDS Human immunodeficiency virus 1 (HIV-1)
SOURCE Human immunodeficiency virus 1
ORGANISM Human immunodeficiency virus 1
Viruses; Retroviridae; Retroviridae; Lentivirus; Primate
lentivirus group.
REFERENCE 1
AUTHORS Watkins, B.A. and Reitz, M.S.
TITLE Human monoclonal antibodies to hiv-1 envelope glycoprotein gp120
JOURNAL Patent: WO 0100678-A 32 04-JAN-2001;
THE GOVERNMENT OF THE UNITED STATES OF AMERICA (US)
LOCATION/Qualifiers
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QY 4 GAGTCTGCCCGCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACTGTCTCT 63
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QY 301 TTGGACAACTGGGCGGAGGAAACCTGGTCAACCGTCTCTCTCA 342
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RESULT 7
HST22X1 411 bp mRNA linear PRI 30-APR-1997
LOCUS H.sapiens mRNA for Ig heavy chain variable region (VH4DJ) (clone
T22.1).
DEFINITION HST22X1
ACCESSION Z75385
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QY 304 GACACTGGGGCCAGGGAACCTGGTCAACCGTCTCTCA 342
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RESULT 9
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 DEFINITION Human immunoglobulin heavy chain variable region (V4-31) gene,
 partial cds.
 ACCESSION U80129
 VERSION U80129.1 GI:1791100
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 360)
 AUTHORS Glas,A.M., Nottenburg,C. and Milner,E.C.
 TITLE Analysis of rearranged immunoglobulin heavy chain variable region
 genes obtained from a bone marrow transplant (BMT) recipient
 JOURNAL Clin. Exp. Immunol. 107 (2), 372-380 (1997)
 MEDLINE 97182739
 PUBMED 9030878
 REFERENCE 2 (bases 1 to 360)
 AUTHORS Glas,A.M., Nottenburg,C. and Milner,E.C.B.
 TITLE Direct Submission
 JOURNAL Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center,
 1000 Seneca Street, Seattle, WA 98101, USA
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RESULT 10

HSU80130 360 bp DNA linear PRI 19-FEB-1997
 LOCUS Human immunoglobulin heavy chain variable region (V4-31) gene,
 partial cds.
 DEFINITION
 ACCESSION U80130
 VERSION U80130.1 GI:1791102
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 360)
 AUTHORS Glas,A.M., Nottenburg,C. and Milner,E.C.
 TITLE Analysis of rearranged immunoglobulin heavy chain variable region
 genes obtained from a bone marrow transplant (BMT) recipient
 JOURNAL Clin. Exp. Immunol. 107 (2), 372-380 (1997)
 MEDLINE 97182739
 PUBMED 9030878
 REFERENCE 2 (bases 1 to 360)
 AUTHORS Glas,A.M., Nottenburg,C. and Milner,E.C.B.
 TITLE Direct Submission
 JOURNAL Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center,
 1000 Seneca Street, Seattle, WA 98101, USA
 FEATURES
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ORIGIN

Query Match 82.7%; Score 283; DB 9; Length 360;
 Best Local Similarity 91.0%; Pred. No. 2.8e-70;
 Matches 314; Conservative 0; Mismatches 25; Indels 6; Gaps 1;
 QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCTGTCCCTCACTGCACTGTCTCT 63
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 Db 16 GAGTCGGGCCAGGACTGGTGAAGCCTTCACAGACCTGTCCCTCACTGCACTGTCTCT 75
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Db 76 GGTGCTCCATCAGCAGTGGTGGTTACTACTGGAGCTGGATCCGCCAGCACCCAGGGAAG 135
 QY 124 GGCCTGGAGTGGATCGGTACATCTATCAGTGSACACACTACAAACCCGTCCTC 183
 Db 136 GGCCTGGAGTGGATCGGTACATCTATCAGTGSACACACTACAAACCCGTCCTC 195
 QY 184 AAGAGTCCAGTATACCATGTAGTAGACAGCTTAAGAACCCTCTCCCTGAGGCTGAGC 243
 Db 196 AAGAGTCCAGTATACCATGTAGTAGACAGCTTAAGAACCCTCTCCCTGAGGCTGAGC 255
 QY 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAG-----GTCCAGATGGGTAC 297
 Db 256 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGGGGTGAGTGGCTGTGATC 315
 QY 298 ACTTTGGACAACTGGGCGCAGGACCGTGTACCGTCTCTCA 342
 Db 316 TATTITGACTACTGGGGCCAGGAACCCCTGTGTCACCGTCTCTCA 360

RESULT 11
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 LOCUS Homo sapiens ID:CLL019 IgM heavy chain variable region mRNA, partial cds.
 DEFINITION AF021954.1 GI:3004697
 ACCESSION Homo sapiens (human)
 VERSION Homo sapiens
 KEYWORDS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 SOURCE Chlorazzi, N.
 ORGANISM Differences in Ig variable region gene use and mutation in IgM vs IgG CLL suggest selection for distinct surface membrane Ig receptors
 REFERENCE 1 (bases 1 to 358)
 AUTHORS Chlorazzi, N.
 TITLE Direct Submission
 JOURNAL Submitted (02-SEP-1997) Medicine, North Shore University Hospital, 350 Community Drive, Manhasset, NY 11030, USA
 FEATURES
 Location/Qualifiers
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 /chromosome="14"
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 /protein_id="AAC09088.1"
 /db_xref="GI:3004698"
 /translation="QVQLQESGPGLVKPSQTLSTLTQVSGSISSGGVYVSWIRQHPG KLEWIGVYVSGSTYNPSLKSRTISVDTSKNQPSLKLSVTAADTAVNYCAKAT VTHFDYWGQSLTVVSS"

CDS

Query Match 82.7%; Score 282.6; DB 9; Length 358;
 Best Local Similarity 91.2%; Pred. No. 3.3e-70;
 Matches 312; Conservative 0; Mismatches 27; Indels 3; Gaps 1;
 QY 4 GAGTCTGCCAGGACTGGTGAAGCCTTCA CAGACCCCTGTCCCTCACTGTCTCT 63
 Db 16 GAGTGGGCCCCAGGACTGGTGAAGCCTTCA CAGACCCCTGTCCCTCACTGTCTCT 75
 QY 64 GGTGCTCCATCCGACGTTGGTATTACTAGGATGGATCCGACGCTCAGGGAG 123
 Db 76 GGTGCTCCATCAGCAGTGGTGGTATTACTAGGATGGATCCGACGCTCAGGGAG 135
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ORIGIN

Query Match 82.4%; Score 281.8; DB 12; Length 403;
 Best Local Similarity 91.2%; Pred. No. 6.3e-70;
 Matches 311; Conservative 0; Mismatches 27; Indels 3; Gaps 1;
 QY 5 AGTCTGCCAGGACTGGTGAAGCCTTCA CAGACCCCTGTCCCTCACTGTCTCTG 64
 Db 42 AGTCTGCCAGGACTGGTGAAGCCTTCA CAGACCCCTGTCCCTCACTGTCTCTG 101
 QY 65 GTGGCTCCATCCGACGTTGGTGGTATTACTAGGATCCGCGACGCTCAGGGAGG 124
 Db 102 GTGGCTCCATCAGCAGTGGTGGTATTACTAGGATCCGCGACACCCAGGGAGG 161
 QY 125 GCTTGGAGTGGATCGGGTACATCTATCAGAGTGCGAAACACTACAAACCCGTCCTCA 184
 Db 162 GCTTGGAGTGGATCGGGTACATCTATCAGAGTGCGAGCACTACTACAAACCCGTCCTCA 221
 QY 185 AGACTCAGATTACCATGTCTAGTAGACAGCTTCTAAGAACCACTTCTCCTGAGGCTGAGCT 244
 Db 222 AGACTCAGATTACCATGTCTAGTAGACAGCTTCTAAGAACCACTTCTCCTGAGGCTGAGCT 281
 QY 245 CTGTGACTGCGCGGACACGCGCGTGTATTACTGTGGG---AGTCAAGTGGGTACACTT 301

Db 136 GGCCTGGAGTGGATGGGTATCATTTACTAGTGGAGCACCTACTACAAACCCGTCCTC 195
 QY 184 AAGAGTCCAGTATACCATGTAGTAGACAGCTTAAGAACCCTCTCCCTGAGGCTGAGC 243
 Db 196 AAGAGTCCAGTATACCATGTAGTAGACAGCTTAAGAACCCTCTCCCTGAGGCTGAGC 255
 QY 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGGTACAGAT---GGGTACACT 300
 Db 256 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCAAGGGAGCTACGTTGACCCAC 315
 QY 301 TTGACAACTGGGCGCAGGGAACCTGTCAACCGTCTCTCA 342
 Db 316 TTGACTACTGGGCGCAGGAACCTGTGTACCGTCTCTCA 357

RESULT 12
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 DEFINITION AF452917
 ACCESSION AF452917
 VERSION AF452917.1 GI:25988060
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 403)
 AUTHORS Weitkamp, J.-H. and Crowe, J.E. Jr.
 TITLE Infant B Cell Repertoires are Sufficiently Diversified for Mature Virus-Specific Responses, but Lack Somatic Mutations
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 403)
 AUTHORS Weitkamp, J.-H. and Crowe, J.E. Jr.
 TITLE Direct Submission
 JOURNAL Submitted (28-NOV-2001) Pediatrics, Vanderbilt University Medical Center, 1161 21st Avenue South, D-7235 Medical Center North, Nashville, TN 37232-2581, USA

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ORIGIN

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 Best Local Similarity 91.2%; Pred. No. 6.3e-70;
 Matches 311; Conservative 0; Mismatches 27; Indels 3; Gaps 1;
 QY 5 AGTCTGCCAGGACTGGTGAAGCCTTCA CAGACCCCTGTCCCTCACTGTCTCTG 64
 Db 42 AGTCTGCCAGGACTGGTGAAGCCTTCA CAGACCCCTGTCCCTCACTGTCTCTG 101
 QY 65 GTGGCTCCATCCGACGTTGGTGGTATTACTAGGATCCGCGACGCTCAGGGAGG 124
 Db 102 GTGGCTCCATCAGCAGTGGTGGTATTACTAGGATCCGCGACACCCAGGGAGG 161
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 Db 162 GCTTGGAGTGGATCGGGTACATCTATCAGAGTGCGAGCACTACTACAAACCCGTCCTCA 221
 QY 185 AGACTCAGATTACCATGTCTAGTAGACAGCTTCTAAGAACCACTTCTCCTGAGGCTGAGCT 244
 Db 222 AGACTCAGATTACCATGTCTAGTAGACAGCTTCTAAGAACCACTTCTCCTGAGGCTGAGCT 281
 QY 245 CTGTGACTGCGCGGACACGCGCGTGTATTACTGTGGG---AGTCAAGTGGGTACACTT 301

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Db      282 CTGTGACTCCGCGACACGCGCGTGTATTACTGTGCGAGCAGGTGGCTACGCGCTGACT 341
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LOCUS   HSA245020
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ACCESSION AJ245020
VERSION  AJ245020.1 GI:4995498
KEYWORDS IGM; IgM heavy chain; immunoglobulin mu heavy chain; variable region.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS   Dono, M., Zupo, S., Leanza, N., Melioli, G., Fogli, M., Melagrana, A.,
          Chiorazzi, N. and Ferrarini, M.
          Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic
          marginal zone equivalents
          J. Immunol. 164 (11), 5596-5604 (2000)
JOURNAL  20281644
MEDLINE  10820234
REFERENCE 2 (bases 1 to 351)
AUTHORS   Dono, M.
          Direct Submission
          Submitted (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca
          sul Cancro, Immunologia Clinica, L.go Rosanna benzi 10- Genova,
          ITALY
FEATURES             Location/Qualifiers
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Matches 310; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

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QY      64 GGTGGCTCCATCCGAGTGTGGTATTACTGTGAGTTGGATCCGCCAGCGTCCAGGGAAG 123
Db      76 GGTGGCTCCATCCGAGTGTGGTATTACTGTGAGTTGGATCCGCCAGCGTCCAGGGAAG 135

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QY      124 GGCCTGGAGTGATCGGGTACATCTATCACAGTGGCAACACACTCAACAACCCGTCCTC 183
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QY      184 AAGAGTCGAGTTACCATGTCTAGTAGACACGCTTAAGAACCATTCTCCCTGAGGCTGAGC 243
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Db      313 GACTACTGGGCGCAGGGAACCCCTGTGTACCGCTCTCCTCA 351

RESULT 14
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LOCUS   HST14X13
DEFINITION H.sapiens mRNA for Ig heavy chain variable region (VH4DJ) (clone
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ACCESSION Z75365
VERSION  Z75365.1 GI:2062027
KEYWORDS immunoglobulin; immunoglobulin heavy chain; immunoglobulin
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SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 414)
AUTHORS   Tonnelie, C., D'Ercole, C., Depraetere, V., Metras, D., Boubli, L. and
          Fougereau, M.
          Human thymic B cells largely overexpress the VH4 Ig gene family. A
          possible role in the control of tolerance in situ?
          Int. Immunol. 9 (3), 407-414 (1997)
JOURNAL  9088979
MEDLINE  97244170
REFERENCE 2 (bases 1 to 414)
AUTHORS   Tonnelie, C.
          Direct Submission
          Submitted (26-JUN-1996) Cecile Tonnelie, Centre d'Immunologie
          Marseille Luminy, Marseille, 13288, France
JOURNAL  Location/Qualifiers
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Best Local Similarity 90.9%; Pred. No. 1.8e-69;
Matches 310; Conservative 0; Mismatches 28; Indels 3; Gaps 1;

QY      4 GAGTCGCGCCAGGACTGTGTGAAGCCTTCACAGACCCCTGTCCTCACTGCACTGTCTCT 63
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 Db 193 GGCTGGAGTGGATCGGGTACATCTATCACAAGTGGAGCACCTACTACAACCCCGTCCCTC 252
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 Db 253 AAGAGTCGAGTTACCATGTCAGTAGACACGCTCTAAGAACCACTTCTCCCTGAGCTGAGC 312
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 Db 313 TCTGTGACTGCCGGGACACGGCCGTGTATCTGTGCGAGTCAAGGGGTGTCCCTTAC 372
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RESULT 15

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 ACCESSION Z75378
 VERSION Z75378.1 GI:2062042
 KEYWORDS immunoglobulin; immunoglobulin heavy chain; immunoglobulin superfamily; variable region.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 414)
 Tonnelle,C., D'Ercole,C., Depraetere,V., Metras,D., Boubli,L. and Fougereau,M.
 Human thymic B cells largely overexpress the VH4 Ig gene family. A possible role in the control of tolerance in situ?
 Int. Immunol. 9 (3), 407-414 (1997)
 JOURNAL 97244170
 MEDLINE 9088979
 REFERENCE 2 (bases 1 to 414)
 AUTHORS Tonnelle,C.
 TITLE Direct Submission
 JOURNAL Submitted (26-JUN-1996) Cecile Tonnelle, Centre d'Immunologie Marseille Luminy, Marseille, 13208, France
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 Best Local Similarity 90.9%; Pred.No. 1.8e-69;
 Matches 310; Conservative 0; Mismatches 28; Indels 3; Gaps 1;
 Qy 4 GAGTCTGGCCAGACTGGTGAAGCCTTTCAGACCCCTGTCCCTCAGCTGACTGTCTCT 63
 Db 73 GAGTCGGGCCAGGAGCTGGTGAAGCCTTTCAGACCCCTGTCCCTCAGCCGACTGTCTCT 132

Qy 64 GGTGGCTCCATCCGACGTGGTGGTTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 123
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 Qy 124 GGCCTGGAGTGGATCGGGTACATCTATCACAAGTGGCAACACCTACAAACCCCGTCCCTC 183
 Db 193 GGCCTGGAGTGGATCGGGTACATCTATCACAAGTGGGAGCACCTACTACAACCCCGTCCCTC 252
 Qy 184 AAGAGTCGAGTTACCATGTCAGTAGACACGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 243
 Db 253 AAGAGTCGAGTTACCATGTCAGTAGACACGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 312
 Qy 244 TCTGTGACTGCCGGGACACGGCCGTGTATCTGTGCGAGTCA---GATGGGTACACT 300
 Db 313 TCTGTGACTGCCGGGACACGGCCGTGTATCTGTGCGAGTCAAGGGGTGTCCCTTAC 372
 Qy 301 TTGGACAACCTGGGGCCAGGGAACCCCTGGTCAACCGTCTCCTC 341
 Db 373 TTTGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCCTC 413

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 Job time : 1472.46 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 00:12:28 ; Search time 2005.71 seconds
(without alignments)
5091.898 Million cell updates/sec

Title: US-10-027-725A-3
Perfect score: 342
Sequence: 1 ctogactgtgcccaggact.....ccctgtgtcacogtctctca 342

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	264	77.2	607	12	BM783015
3	261.4	76.4	677	12	BG686767
4	258.8	75.7	509	10	AW406349

5	257.8	75.4	490	14	CD689564
6	256.6	75.0	369	10	AW404242
7	254	74.3	643	9	AU134293
8	252.6	73.9	1108	12	BM920469
9	250	73.1	977	13	BM920469
10	250	73.1	1201	13	BM920469
11	249.8	73.0	914	12	BM920469
12	248.4	72.6	890	13	BM920469
13	248	72.5	904	13	BM920469
14	246.4	72.0	447	10	AW402200
15	246.2	72.0	725	12	BG431274
16	246.2	72.0	959	13	BG431274
17	246	71.9	813	13	BG431274
18	245.8	71.9	582	10	AW401348
19	245.8	71.9	1050	9	AL552672
20	244.8	71.6	363	10	AW403420
21	244.6	71.5	903	13	BG706579
22	244.2	71.4	814	12	BG685325
23	244.2	71.4	828	10	BF974568
24	244	71.3	421	10	AW407630
25	243.8	71.3	856	13	BQ421299
26	241.6	70.6	542	10	AW951834
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29	241.4	70.6	474	10	AW408410
30	241.4	70.6	924	13	BQ708516
31	240.6	70.4	368	10	AW403989
32	240.2	70.2	921	13	BQ710000
33	240.2	70.2	939	13	BQ708070
34	239.8	70.1	915	13	BQ706358
35	239.8	70.1	1201	13	EX417108
36	239.4	70.0	924	12	BG758027
37	239.4	70.0	942	13	BQ706244
38	239.4	70.0	1201	13	BX380759
39	239.2	69.9	856	12	BG757400
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sequence.
ACCESSION AU122174
VERSION AU122174.1 GI:10937409
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 832)
AUTHORS Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
Isogai, T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project: 5' - & 3' - end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of

Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

FEATURES

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DEFINITION 5', mRNA sequence.

ACCESSION BM783015
VERSION BM783015.1 GI:19131247
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 607)
AUTHORS Kim N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.

21C Frontier Korean EST Project 2001

Unpublished (2002)

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 2 row: E column: 06

High quality sequence stop: 607.

FEATURES

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/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F, by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

ORIGIN

Query Match 77.2%; Score 264; DB 12; Length 607;
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QY 64 GGTGCTCCATCCGAGTGGTGGTTACTTACTGGAGTTGGATCGCCAGGCTCCAGGAG 123
DB 172 GGTGCTCCATGAAACAGTGGTAGTTACTTGGAGTGGATCGCCCAACACCCAGGAG 231
QY 124 GGCCTGGAGTGGATCGGTACATCTATCAGTGGCAACACCTTACAAACCCGTCCTC 183
DB 232 GGCCTGGAGTGGATCGGTACATCTATCAGTGGCAACACCTTACAAACCCGTCCTC 291
QY 184 AAGAGTCGAGTTACCATGTCACTAGACAGCTCTAAGAACCCTTCTCCCTGAGGCTGAGC 243
DB 292 AAGAGTCGAGTTACCATGTCACTAGACAGCTCTAAGAACCCTTCTCCCTGAGGCTGAGC 351
QY 244 TCTGTGACTGCGCGGACACGCGCGGTGTTACTTACTGTGCGAG-----GTGAGTGGG 294
DB 352 TCTGTGACTGCGCGGACACGCGCGGTGTTACTTACTGTGCGAGATGGCAATTACGATA 411
QY 295 TACACTTTGGCAACCTGGGCGCAGGAAACCTTGGTCAACCGTCTCTCA 342
DB 412 TACGGTATGGAGCTGTGGGGCCAGGACCGGTCAACCGTCTCTCTCA 459

RESULT 3

BM786767

LOCUS

DEFINITION

BM786767.1

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 677)

AUTHORS NIH-MGC

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

BM786767 677 bp mRNA linear EST 01-MAY-2001
602650737F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4763217 5',
mRNA sequence.

BM786767

BM786767.1

EST.

Homo sapiens

Homo sapiens

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 677)

AUTHORS NIH-MGC

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: L1CM1618 row: i column: 10
 High quality sequence stop: 675.
 Location/Qualifiers

FEATURES

```

1..677
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4763217"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/notes="Organ: B-cells; Vector: pORF7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

```

ORIGIN

```

Query Match      76.4%; Score 261.4; DB 12; Length 677;
Best Local Similarity 89.0%; Pred. No. 1.1e-58;
Matches 307; Conservative 0; Mismatches 31; Indels 7; Gaps 2;

Qy 4 GAGTCTGCCAGGACTGGTGAAGCCTTCACAGACCCCTGCTCCCTCAGCTGCTCTCT 63
    |||||
Db 99 GAGTCGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGCTCCCTCAGCTGCTCTCT 158
    |||||

Qy 64 GGTGGCTCCATCCGACGFTGGTGTATTACTGGAGTTGGATCCGCGACGTCACAGGGAAG 123
    |||||
Db 159 GGTGGCTCCATCAGCAGTGGTGGTTACTACTGGAGTGGATCCGCGACACCCCA-GGAAG 217
    |||||

Qy 124 GGCTGGAGTGGATCGGGTACATCTATCAGTGGCAACACCTACACAAACCCGTCCTC 183
    |||||
Db 218 GGCTGGAGTGGATGGGTGATCTATTACAGTGGGAGCCTACTACTCAACCCGTCCTC 277
    |||||

Qy 184 AAGAGTCGAGTTACATGTCAGTACACGCTCTAAGAACCACTTCTCCCTCAGCTGAGC 243
    |||||
Db 278 AAGAGTCGAGTTACATGTCAGTACACGCTCTAAGAACCACTTCTCCCTCAGCTGAGC 337
    |||||

Qy 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGA-----GGTCAGATGGGTAC 297
    |||||
Db 338 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGATCGCAAGAGAGGAGGC 397
    |||||

Qy 298 ACTTTGGACACTGGGGCCAGGGAACCTGTGTCACCGTCTCTCTCA 342
    |||||
Db 398 GGGTTGACCCCTGGGGCCAGGGAACCTGTGTCACCGTCTCTCTCA 442
    |||||

```

```

RESULT 4
AW406349
LOCUS
DEFINITION
UI-HF-BLO-aco-h-03-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3059933 5', mRNA sequence.
AW406349
ACCESSION
VERSION
AW406349.1 GI:6925406
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 509)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
TITLE
Contact: Robert Strausberg, Ph.D.
COMMENT
Email: cgapbs-r@mail.nih.gov

```

Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrip/image/image.html
 Seq primer: M13 Forward.

FEATURES

```

Location/Qualifiers
1..509
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3059933"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH_MGC_37"
/notes="vector: p77T3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

```

ORIGIN

```

Query Match      75.7%; Score 258.8; DB 10; Length 509;
Best Local Similarity 86.8%; Pred. No. 4.7e-58;
Matches 297; Conservative 0; Mismatches 42; Indels 3; Gaps 1;

Qy 4 GAGTCTGCCAGGACTGGTGAAGCCTTCACAGACCCCTGCTCCCTCAGCTGCTCTCT 63
    |||||
Db 54 GAGTCGGGCCAGGACTGGTGAAGCCTTCGAGACCCCTGCTCCCTCAGCTGCTCTCT 113
    |||||

Qy 64 GGTGGCTCCATCCGACGFTGGTGTATTACTGGAGTTGGATCCGCGACGTCACAGGGAAG 123
    |||||
Db 114 GGTGGCTCCATCAGCAGTGGTGTATTACTGGAGTGGATCCGCGACCCCAAGGGAAG 173
    |||||

Qy 124 GGCTGGAGTGGATCGGGTACATCTATCAGTGGCAACACCTACACAAACCCGTCCTC 183
    |||||
Db 174 GGCTGGAGTGGATGGGAGTATCTATTATAGTGGGAGCCTACTACTCAACCCGTCCTC 233
    |||||

Qy 184 AAGAGTCGAGTTACATGTCAGTACACGCTCTAAGAACCACTTCTCCCTCAGCTGAGC 243
    |||||
Db 234 AAGAGTCGAGTTACATGTCAGTACACGCTCTAAGAACCACTTCTCCCTCAGCTGAGC 293
    |||||

Qy 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAG-----GTGAGATGGGTACT 300
    |||||
Db 294 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGACCTCTCTACGAGACCTGG 353
    |||||

Qy 301 TTGGACAACCTGGGGCCAGGGAACCCGTGTGTCACCGTCTCTCTCA 342
    |||||
Db 354 TTCGACCCCTGGGGCCAGGGAACCCGTGTGTCACCGTCTCTCTCA 395
    |||||

```

```

RESULT 5
CD689564
LOCUS
DEFINITION
EST6087 human nasopharynx Homo sapiens cDNA, mRNA sequence.
CD689564
ACCESSION
CD689564.1 GI:32209443
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 490)
Zeng,Y.-X.
Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
Zeng,Y.-X.
Transcriptional Gene Expression Profile of Human Nasopharynx
Unpublished (2003)
JOURNAL
COMMENT
Contact: Yixin Zeng

```

Cancer Center
Sun Yat-sen University
651 DongFeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@zsums.edu.cn.

FEATURES
source
1. 490
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cdna library from southern Chinese"

ORIGIN

Query Match 75.4%; Score 257.8; DB 14; Length 490;
Best Local Similarity 86.8%; Pred. No. 8.6e-58;
Matches 296; Conservative 0; Mismatches 42; Indels 3; Gaps 1;
QY 5 AGCTGCCCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACCTGCTCTG 64
DB 111 AGTCGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACCTGCTCTG 170
QY 65 GTGGCTCCATCCGACGTGGTGGTTATTACTGAGTTGGATCCGCCAGCGTCCAGGAAGG 124
DB 171 GTGACTCCATCAGCAGTGTGGTTACTACTGAGTTGGATTGCCAGCACCCAGGAAGG 230
QY 125 GCCTGAGTGGATCGGGTACATCTATCAGTGGCAACACCTPACAAACCCGTCCTCA 184
DB 231 GCCTGAGTGGATCGGGTACATCTATCAGTGGGAGTCCGACTACACCCGTCCTCA 290
QY 185 AGAGTCGAGTTACCATGTCTAGTAGACAGCTTAAGAACCACTTCCCTGAGGCTGAGCT 244
DB 291 AGAGTCGAGTTACCATGTCTAGTAGACAGCTTAAGAACCACTTCCCTGAGGCTGAGGT 350
QY 245 CTGTGACTGCCCGGACAGCGCGTGTATTACTGCGAGGTTCAGAT---GGGTACACTT 301
DB 351 CTGTGACGCGCGGACAGCGCGCTATATTACTGCGAGAGTGGTCCCGACGATTAA 410
QY 302 TGGACAACTGGGGCAGGGAACCCCTGGTCAACCGTCTCTCA 342
DB 411 TTGACTACTGGGGCAGGGAATCCTGGTCACCGTCTCTCA 451

RESULT 6

AW404242
LOCUS
DEFINITION
UI-HF-BLO-abq-f-09-0-UI.r1 NIH_MGC 37 Homo sapiens cdna clone
IMAGE:3057545 5', mRNA sequence.
ACCESSION
AW404242.1 GI:6923299
VERSION
EST.
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 369)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cdna Library Preparation: M.B. Soares Lab
cdna Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www.bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES
source

Location/Qualifiers
1. 369
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone_lib="IMAGE:3057545"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH_MGC_37"
/note="Vector: p7T3-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 75.0%; Score 256.6; DB 10; Length 369;
Best Local Similarity 87.8%; Pred. No. 1.5e-57;
Matches 280; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACCTGCTCT 63
DB 34 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACCTGCTCT 93
QY 64 GGTGGCTCATCCGACGTGGTGGTTATTACTGGAGTTGGATCCGCCAGCGTCCAGGAAG 123
DB 94 GGTGGCTCATCAGCAGTGTGGTTACTACTGGAGTTGGATCCGCCAGCACCCAGGAAG 153
QY 124 GGCCTGGAGTGGATCGGGTACATCTATCAGTGGCAACACCTPACAAACCCGTCCTTC 183
DB 154 GGCCTGGAGTGGATCGGGTACATCTATAACAGTGGGAGCACCTACTACAAACCCGTCCT 213
QY 184 AGAGTCGAGTTACCATGTCTAGTAGACAGCTTAAGAACCACTTCCCTGAGGCTGAGC 243
DB 214 AGAGTCGAGTTACCATGTCTAGTAGACAGCTTAAGAACCACTTCCCTGAGGATGAGC 273
QY 244 TCTGTGACTGCCCGGACAGCGCGTGTATTACTGCGAGGTTCAGATGGGTACACTTTG 303
DB 274 TCTGTGACTGCCCGGACAGCGCGTGTATTACTGCGAGATCTTTGGCGTATTACTTT 333
QY 304 GACAACTGGGGCCAGGGA 322
DB 334 GATAGTAGTGGTTACGGAA 352

RESULT 7

AUI34293
LOCUS
DEFINITION
OVARC1 Homo sapiens cdna clone OVARC1001672 5', mRNA
sequence.
ACCESSION
AUI34293
VERSION
AUI34293.1 GI:10994832
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 643)
Ota.T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
HRI human cdna project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cdna project; 5'- & 3'-end one pass sequencing: Helix

Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute

FEATURES

Location/Qualifiers
1..643

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="OVARC1001672"
/tissue_type="ovary, tumor tissue"
/clone_lib="OVARC1"
/note="Vector: pME18SFL3"

ORIGIN

```

Query Match      74.3%; Score 254; DB 9; Length 643;
Best Local Similarity 85.1%; Pred. No. 1e-56;
Matches 303; Conservative 0; Mismatches 35; Indels 18; Gaps 1;

QY 5 AGTGTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACCTGTCTCTG 64
   |||||
Db 110 AGTGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACCTGTCTCTG 169

QY 65 GTGGCTCATCGGAGTGGTGTATTACTGGAGTTGGATCGCCAGCGTCCAGGGAAG 124
   |||||
Db 170 GTGGCTCATCAGCAGTGGTGTATTACTTGGACCTGGATCGCCCAACACCCAGGGAAG 229

QY 125 CCCTGGAGTGGATCGGTACATCTATCACAGTGGCAACACCTACACACCGTCCCTCA 184
   |||||
Db 230 CCCTGGAGTGGATGGGTACATCTATTACAGTGGGACCACTTACTACAAACCGTCCCTCA 289

QY 185 AGAGTCGAGTTACCATGTGCTAGTAGACAGTCTTAAGAACCCACTTCTCCCTGAGGCTGAGCT 244
   |||||
Db 290 AGAGTCGAGTTACCATGTGCTAGTAGACAGTCTTAAGAACCCACTTCTCCCTGAGGCTGAGG 349

QY 245 CTGTGACTGCGCGGACACGCGCGTGTATTACTGTGGAGTTCAGATGGGTACAT---- 300
   |||||
Db 350 CTGTGACTGCGCGGACACGCGCGTGTATTACTGTGGAGTTCAGATGGGTACATTAAGTG 409

QY 301 -----TTGGACAACTGGGCGGAGGACCCCTGGTACCGTCTCCCTCA 342
   |||||
Db 410 GGACCTACAGTAAGTTGACCACCTGGGCGGAGGAAACCCCTGTACCGTCTCCCTCA 465

```

RESULT 8
BM920469
LOCUS
DEFINITION
AGENCOURT_6709612 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5750444
5', mRNA sequence.

ACCESSION
BM920469
VERSION
BM920469.1 GI:19370848

KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 1108)
NIH-MGC <http://mgi.nci.nih.gov/>.

AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

TITLE
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

JOURNAL
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.

COMMENT
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: L14M12781 row: g column: 21
High quality sequence stop: 626.

FEATURES

Location/Qualifiers
1..1108

/organism="Homo sapiens"

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5750444"
/lab_host="DH10B"

/clone_lib="NIH_MGC_122"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed, and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."

ORIGIN

```

Query Match      73.9%; Score 252.6; DB 12; Length 1108;
Best Local Similarity 85.5%; Pred. No. 3.2e-56;
Matches 295; Conservative 0; Mismatches 44; Indels 6; Gaps 1;

QY 4 GAGTGTGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACCTGTCTCT 63
   |||||
Db 110 GAGTGGGCCAGGACTGGTGAAGCCTTCGGAGACCCCTGTCCCTCACCTGCACCTGTCTCT 169

QY 64 GGTGCTCCATCCGAGTGGTGTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 123
   |||||
Db 170 GGTGCTCCGTCAGCAGTGGTAGTACTACTGGAGTGGATCCGCCAGCGTCCAGGGAAG 229

QY 124 GGCCTGGAGTGGATCGGGTACATCTATCACAGTGGCAACCTACACAAACCCGTCCTC 183
   |||||
Db 230 GGACTGGAGTGGATGGGTATTATCTATTACAGTGGGACCACTACACCCCTCCCTC 289

QY 184 AAGAGTCGAGTTACCATGTGCTAGTAGACAGTCTTAAGAACCCACTTCTCCCTGAGGCTGAGC 243
   |||||
Db 290 AAGAGTCGAGTCAACCATATCAGTAGACAGTCCCAAGAACCACTTCTCCCTGAAGCTGAGC 349

QY 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGGAGTTCAGATGGG-----TAC 297
   |||||
Db 350 TCTGTGACCGCTGCGGACACGCGCGTGTATTACTGTGGAGTTCAGATGGGCGGGGACTAC 409

QY 298 ACTTTGGACAACTGGGCGGAGGAAACCCCTGTACCGTCTCCCTCA 342
   |||||
Db 410 TACATGGAGCTCTGGGCGCAAGGGACCGTCAACCGTCTCCCTCA 454

```

RESULT 9

BM9396901
LOCUS

DEFINITION
BM9396901 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1026YB08 5-PRIME, mRNA sequence.

ACCESSION
BM9396901

VERSION
BM9396901.1 GI:30625036

KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens

REFERENCE
1 (bases 1 to 977)

AUTHORS
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.

TITLE
Full-length cDNA libraries and normalization
Unpublished (2001)

COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7198.r For
more information about this cluster, see
<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0D1026B04QPI&cluster=7198.r> Contact :
Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DI026BC04QPl.

FEATURES
source

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1..977
Location/Qualifiers
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="CS0DI026YR08"
  /tissue_type="PLACENTA COT 25-NORMALIZED"
  /note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
```

ORIGIN

```
Query Match      73.1%; Score 250; DB 13; Length 977;
Best Local Similarity 84.5%; Pred. No. 1.5e-55;
Matches 299; Conservative 0; Mismatches 40; Indels 15; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGCTCCCTCACCTGCACCTGTCTCT 63
Db 163 GAGTGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGCTCCCTCACCTGCACCTGTCTCT 222
QY 64 GGTGGCTCCATCGCAGTGGTGTATTACTGGAGTTGGATCGCGCAGCGTCCAGGGAAG 123
Db 223 GGTGGCTCCATCAGCAGTGGTGTATTACTGGAGTTGGATCGCGCAGCGCGCGGAAG 282
QY 124 GGCCTGGAGTGATCGGGTACATCTATCAGCTGGCAACACCTACAGACCCGCTCCCTC 183
Db 283 GGACTGGAGTGGATGGGGGTATCTATACCACTGGGAGCACCACCACTACAAACCCCTCCCTC 342
QY 184 AAGAGTCGAGTTACCATGTCAGTAGACAGTCTTAAGAACCATCTCCCTGAGGCTGAGC 243
Db 343 AAGAGTCGAGTTACCATGTCAGTAGACAGTCTTAAGAACCATCTCCCTGAGGCTGAGC 402
QY 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGA-----GGTCA 288
Db 403 TCTGTGACCGCGCAGACACGCGCGTGTATTACTGTGCGATCACCAGCATAGTGGCTAC 462
QY 289 GATGGGTACACTTTGACACACTGGGGCCAGGNAACCTGGTCAACCGTCTCCCTCA 342
Db 463 GATGAGGGTGTGTTGACTACTGGGGCCAGGNAACCTGGTCAACCGTCTCCCTCA 516
```

RESULT 10

```

BX336959
LOCUS
DEFINITION
BX336959 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI034YI02 5-PRIME, mRNA sequence.
ACCESSION
BX336959.1 GI:30341572
VERSION
BX336959
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li W.B., Gruber C., Jessee J. and Polayes D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7198.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI034BE01QPl&cluster=7198.r. Contact :
Peng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI034BE01QPl.
Location/Qualifiers
```

FEATURES

source

```
1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI034YI02"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
```

ORIGIN

```
Query Match      73.1%; Score 250; DB 13; Length 1201;
Best Local Similarity 84.5%; Pred. No. 1.7e-55;
Matches 299; Conservative 0; Mismatches 40; Indels 15; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGCTCCCTCACCTGCACCTGTCTCT 63
Db 156 GAGTGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGCTCCCTCACCTGCACCTGTCTCT 215
QY 64 GGTGGCTCCATCGCAGTGGTGTATTACTGGAGTTGGATCGCGCAGCGTCCAGGGAAG 123
Db 216 GGTGGCTCCATCAGCAGTGGTGTATTACTGGAGTTGGATCGCGCAGCGCGCGGAAG 275
QY 124 GGCCTGGAGTGATCGGGTACATCTATCAGCTGGCAACACCTACAGACCCGCTCCCTC 183
Db 276 GGACTGGAGTGGATGGGGGTATCTATACCACTGGGAGCACCACCACTACAAACCCCTCCCTC 335
QY 184 AAGAGTCGAGTTACCATGTCAGTAGACAGTCTTAAGAACCATCTCCCTGAGGCTGAGC 243
Db 336 AAGAGTCGAGTTACCATGTCAGTAGACAGTCTTAAGAACCATCTCCCTGAGGCTGAGC 395
QY 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGA-----GGTCA 288
Db 396 TCTGTGACCGCGCAGACACGCGCGTGTATTACTGTGCGATCACCAGCATAGTGGCTAC 455
QY 289 GATGGGTACACTTTGACACAACTGGGGCCAGGNAACCTGGTCAACCGTCTCCCTCA 342
Db 456 GATGAGGGTGTGTTGACTACTGGGGCCAGGNAACCTGGTCAACCGTCTCCCTCA 509
```

RESULT 11

```

BG757054
LOCUS
DEFINITION
BG757054 602710478F1 NTH_MGC_48 Homo sapiens cDNA clone IMAGE:4850851 5',
mRNA sequence.
ACCESSION
BG757054.1 GI:14067707
VERSION
BG757054
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 914)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Louis W. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI692 row: 1 column: 20
High quality sequence stop: 854.
Location/Qualifiers
1..914
/organism="Homo sapiens"
/mol_type="mRNA"
```



```
/db_xref="taxon:9606"
/clone="IMAGE:4850851"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/notes="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected 500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
```

ORIGIN

```
Query Match 73.0%; Score 249.8; DB 12; Length 914;
Best Local Similarity 86.7%; Pred. No. 1.6e-55;
Matches 301; Conservative 0; Mismatches 37; Indels 9; Gaps 2;

QY 4 GAGCTGCGCCGAGACTGGTGAAGCCTTCACAGACCCCTGCCCTCAGCTGACTGTCTCT 63
Db 93 GAGTGGGGCCGAGACTGGTGAAGCCTTCACAGACCCCTGCCCTCAGCTGACTGTCTCT 152
QY 64 GGTGGCTCCATCCCGCAGTGGTGGTTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 123
Db 153 GGTGGCTCCATCAGCAGTGGTGGTTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 211
QY 124 GGCTGAGTGGATCGGGTACATCTATCAGAGTGGCAACACCTTACAAACCCCGTCCCTC 183
Db 212 GGCTGAGTGGATCGGGTACATCTATCAGAGTGGCAACACCTTACAAACCCCGTCCCTC 271
QY 184 AAGAGTCAGTTACCATGTCTAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGCTGAGC 243
Db 272 AAGAGTCAGTTACCATGTCTAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGCTGAGC 331
QY 244 TCTGTGACTCGCGGACACGGCCGTGTATTACTGTGGAGTTCAGATGGGTACACTTTG 303
Db 332 TCTGTGACTCGCGGACACGGCCGTGTATTACTGTGGAGTTCAGATGGGTACACTTTG 391
QY 304 GACAACT-----GGGGCCAGGGAACCCCTGGTCAACCGTCTCTCA 342
Db 392 CACGACTTTGACTACTGGGGCCAGGAACCCCTGGTCAACCGTCTCTCA 438
```

RESULT 12

```
EX324929
LOCUS BX324929 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0DI086YJ13 5-PRIME, mRNA sequence.
ACCESSION BX324929
VERSION BX324929.1 GI:30338413
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 890)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7198.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0AI086CE07QPI&cluster=7198.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0AI086CE07QPI.
```

FEATURES
source

```
Location/Qualifiers
1..890
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI086YJ13"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
```

ORIGIN

```
Query Match 72.6%; Score 248.4; DB 13; Length 890;
Best Local Similarity 84.2%; Pred. No. 3.7e-55;
Matches 298; Conservative 0; Mismatches 41; Indels 15; Gaps 1;

QY 4 GAGTCTGCGCCGAGACTGGTGAAGCCTTCACAGACCCCTGCCCTCAGCTGACTGTCTCT 63
Db 133 GAGTGGGGCCGAGACTGGTGAAGCCTTCGAGACCCCTGTCCCTCAGCTGACTGTCTCT 192
QY 64 GGTGGCTCCATCCCGCAGTGGTGGTTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 123
Db 193 GGTGGCTCCATCAGCAGTAGTACTTACTACTGGGGCTGGATCCGCCAGCGTCCAGGGAAG 252
QY 124 GGCTGAGTGGATCGGGTACATCTATCAGAGTGGCAACACCTTACAAACCCCGTCCCTC 183
Db 253 GGCTGAGTGGATCGGGTACATCTATCAGAGTGGCAACACCTTACAAACCCCGTCCCTC 312
QY 184 AAGAGTCAGTTACCATGTCTAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGCTGAGC 243
Db 313 AAGAGTCAGTTACCATGTCTAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGCTGAGC 372
QY 244 TCTGTGACTCGCGGACACGGCCGTGTATTACTGTGGAGTTCAGATGGGTACACTTTG 293
Db 373 TCTGTGACTCGCGGACACGGCCGTGTATTACTGTGGAGTTCAGATGGGTACACTTTG 432
QY 294 -----GTACACTTTGGACAACCTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCA 342
Db 433 TGCTACCTCGCCTTTGACTACTGGGGCCAGGAACCCCTGGTCAACCGTCTCTCA 486
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RESULT 13

```
EX324929
LOCUS BX324929 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0DI086YJ13 5-PRIME, mRNA sequence.
ACCESSION BX324929
VERSION BX324929.1 GI:21849387
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 904)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: Agencourt Bioscience Corporation
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM2465 row: k column: 02
High quality sequence stop: 728.
Location/Qualifiers
1..904
/organism="Homo sapiens"
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/mol_type="mRNA"  
/db_xref="taxon:9606"  
/clone="IMAGE:6278137"  
/lab_host="DH10B (phage-resistant)"  
/clone_lib="NIH_MGC_113"  
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGGAG(G). Library constructed by Ling Hong in the  
laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH_MGC Library."
```

ORIGIN

```
Query Match 72.5%; Score 248; DB 13; Length 904;  
Best Local Similarity 84.5%; Pred. No. 4.8e-55;  
Matches 294; Conservative 0; Mismatches 45; Indels 9; Gaps 1;  
  
QY 4 GAGTCTGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACCTGCTCTCT 63  
DB 86 GAGTCTGCCAGGACTGGTGAAGCCTTCGGAGACCCCTGTCCTCACCTGCACCTGCTCTCT 145  
  
QY 64 GGTGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGGATCCGCGAGCGTCCAGGGAAG 123  
DB 146 GGTGCTCCATCAGCAGTAGTAGTTACTACTGGGCTGGATCCGCGAGCGCCCGAGGAAG 205  
  
QY 124 GGCCTGGAGTGGATCGGTACATCTATCAGAGTGCACACCTACACACCCGTCCTC 183  
DB 206 GGGCTGGAGTGGATGGGAGTAGTATTATATAGTGGAGCACCCTACTACACCCGTCCTC 265  
  
QY 184 AAGAGTCGAGTTACCATGTCAGTAGACACGCTTAAGAACCCCTGTCCTCGAGGCTGAGC 243  
DB 266 AAGAGTCGAGTCACCATATCCGTAGACAGCTTCAGAGACCCAGTTCTCCCTGAGCTGAGC 325  
  
QY 244 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGGAGTGTGAG-----TGGG 294  
DB 326 TCTGTGACCGCGGACACGCGCTGTATTACTGTGGAGAGCAGCAGCAGCTGGTA 385  
  
QY 295 TACACTTTGGACAACTGGGCGCAGGACCCCTGTGTCACCGTCTCTCA 342  
DB 386 CATTAATTCCAGCATGGGCGCAGGCGACCCCTGGTCAACCGTCTCTCA 433
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RESULT 14  
AW402200  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 447)  
NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-re@mail.nih.gov  
Eco RI site shown at the beginning of the sequence.  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: M.B. Soares Lab  
DNA Sequencing by: M.B. Soares Lab  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bbrp/image/image.html  
Seq primer: M13 Forward  
Location/Qualifiers  
1. .447
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/organism="Homo sapiens"  
/mol_type="mRNA"  
/db_xref="taxon:9606"  
/clone="IMAGE:3054785"  
/lab_host="DH10B (lymph)"  
/cell_type="germinal center B cells"  
/tissue_type="lymph"  
/cell_line="MGC85"  
/lab_host="DH10B (LTI)"  
/clone_lib="NIH_MGC_36"  
/note="Vector: p7713-Pac; Site 1: NotI; Site 2: Eco RI;  
Constructed from size fractionated cytoplasmic mRNA  
(0.5-1.5kb). Directionally cloned. Cells provided by Louis  
M. Staudt, Ph.D. Library preparation by Maria de Fatima  
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
```

ORIGIN

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Query Match 72.0%; Score 246.4; DB 10; Length 447;  
Best Local Similarity 84.2%; Pred. No. 8.7e-55;  
Matches 293; Conservative 0; Mismatches 46; Indels 9; Gaps 1;  
  
QY 4 GAGTCTGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACCTGCTCTCT 63  
DB 47 GAGTCTGCCAGGACTGGTGAAGCCTTCGGAGACCCCTGTCCTCTCTGCACTGCTCTCT 106  
  
QY 64 GGTGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGGATCCGCGAGCGTCCAGGGAAG 123  
DB 107 GGTGCTCCATCAGCAGGAGTAGTTATTACTGGGCTGGATCCGCGAGCGCCCGAGGAAG 166  
  
QY 124 GGCCTGGAGTGGATCGGTACATCTATCAGAGTGCACACCTACACACCCGTCCTC 183  
DB 167 GGGCTGGAGTGGATGGGAGTAGTATTATATAGTGGAGCACCCTACTACACCCGTCCTC 226  
  
QY 184 AAGAGTCGAGTTACCATGTCAGTAGACACGCTTAAGAACCCCTGTCCTCGAGGCTGAGC 243  
DB 227 AAGAGTCGAGTCACCATATCAATAGACACGCTCCAGAGTACGTTCTCTGAGCTGAGC 286  
  
QY 244 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGAG-----GTCAATGGG 294  
DB 287 TCTGTGACCGCGGACACGCGCTGTATTACTGTGCGAGAGGAGGATGTTGTGTCT 346  
  
QY 295 TACACTTTGGACAACTGGGCGCAGGACCCCTGTGTCACCGTCTCTCA 342  
DB 347 CACTGTTCCAGCCCTGGGCGCAGGGAACCTGGTCAACCGTCTCTCA 394
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RESULT 15  
BG431274  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 725)  
NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-re@mail.nih.gov  
Tissue Procurement: CLONTECH Laboratories, Inc.  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLNL1363 row: h column: 12  
High quality sequence stop: 716.  
Location/Qualifiers
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FEATURES

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4613435"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 75"
/note="Organ: kidney; Vector: PDNR-LIB (Clontech); Site:1;
SfiI (ggccattatggcc); Site:2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGGCGGCACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH MGC Library."

ORIGIN

Query Match 72.0%; Score 246.2; DB 12; Length 725;
Best Local Similarity 82.9%; Pred. No. 1.3e-54;
Matches 281; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
Qy 4 GAGTCTGCGCCAGGACTGGTGAAGCCTTTCACAGACCCCTGTCCTCCCTCACCTGCACCTGTCTCT 63
Db 109 GAGTCGGGCCCAAGACTGGTGAAGCCTTTCGGGGACCCCTGTCCTCCCTGCACCTGTCTCT 168
Qy 64 GGTGGCTCCATCCGCGAGTGGTGGTTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 123
Db 169 GGTGGCTCCATCATCAGTCCCATTTATTACTGGGGCTGGATCCGCCAGCCGCCAGGGAAG 228
Qy 124 GGCCTGGAGTGGATCGGTATCTATCACAGTGGCAACCTACACACCCGTCCTC 183
Db 229 GGGCTGGAGTGGATTGCCAGTATCTCTCACAGTGGGACCACTACTACACCCGTCCTC 288
Qy 184 AAGAGTCGAGTTACCATGTCAAGTACAGACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db 289 GAGAGTCGAGTCACCATATCCGTAGACACGTCACAGAACCACTTCTCCCTGAGGCTGAGG 348
Qy 244 TCTGTGACTGCGCGGACACGCGCGTGTTATTACTGTGCGAGGTGAGATGGGTACACTTTG 303
Db 349 CCTGTGACCGCGCAGACACGCTCTGTATATTATTGTGCGAGATTACTCGGGGGGAGTTT 408
Qy 304 GACAACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA 342
Db 409 GACTATTGGGGCCAGGGAACCCCTGGTCGCGTCTCCTCA 447

Search completed: August 13, 2004, 07:13:20
Job time : 2006.71 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 12, 2004, 11:40:47 ; Search time 222.818 Seconds
(without alignments)
6520.490 Million cell updates/sec

Title: US-10-027-725A-3
Perfect score: 342
Sequence: 1 ctgagctcgtggccaggact.....ccctggtcaccgctctctctca 342

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373663 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	338.8	99.1	342	6	ABK89639 DNA encod
2	322.8	94.4	342	6	ABK89638 DNA encod
3	308.4	90.2	342	6	ABK89637 DNA encod
4	284.6	83.2	352	9	ADC99786 Anti-huma
5	284.6	83.2	352	9	ADD05390 Anti-MUC1
6	284.4	83.2	360	4	Aaf29076 Human HIV
7	275	80.4	352	9	ADC99778 Anti-huma
8	275	80.4	352	9	ADD05382 Anti-MUC1
9	273.8	80.1	369	4	Aaf29046 Human HIV
10	268.4	78.5	358	9	ADC99798 Anti-huma
11	268.4	78.5	358	9	ADD05402 Anti-MUC1
12	267.2	78.1	516	3	AAA46876 DNA encod
13	264	77.2	366	4	Aaf29066 Human HIV
14	263.6	77.1	357	2	AAQ38670 MAB GAH v
15	262.8	76.8	352	9	ADC99806 Anti-huma
16	262.8	76.8	352	9	ADD05410 Anti-MUC1
17	261.4	76.4	741	3	Aaz28998 Anti-muri
18	258.6	75.6	1644	2	Aaz24434 Human bla
19	257	75.1	324	4	ABS46332 Human liv
20	257	75.1	340	6	ABK84446 Human cDN
21	257	75.1	340	7	ACA64884 Human Ig
22	257	75.1	631	2	AAQ78969 Human imm
23	255.8	74.8	450	2	Aax90024 Human mon

ALIGNMENTS

RESULT 1

ABK89639	ID	ABK89639 standard; DNA; 342 BP.
XX	AC	ABK89639;
XX	DT	21-OCT-2002 (first entry)
XX	DE	DNA encoding human IgE Fab clone 100 heavy chain.
XX	KW	Human; fab; ds; gene; antiallergic; vaccine; grass pollen; Phi p 2;
KW	KW	timothy grass pollen allergen; passive immunotherapy.
XX	OS	Homo sapiens.
XX	Key	Location/Qualifiers
FT	CDS	1..342
FT		/*tag= a
FT	misc_feature	/product= "Fab clone 100 heavy chain"
FT		7..78
FT		/*tag= b
FT	misc_feature	/note= "PR1 region"
FT		79..99
FT		/*tag= c
FT	misc_feature	/note= "CDR1 region"
FT		100..123
FT		/*tag= d
FT	misc_feature	/note= "PR2 region"
FT		134..141
FT		/*tag= e
FT	misc_feature	/note= "PR3 region"
FT		142..189
FT		/*tag= f
FT	misc_feature	/note= "CDR2 region"
FT		190..285
FT		/*tag= g
FT	misc_feature	/note= "PR3 region"
FT		286..309
FT		/*tag= h
FT	misc_feature	/note= "CDR3 region"
FT		310..342
FT		/*tag= i
FT	misc_feature	/note= "PR4 region"
PN		WO200253595-A1.

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PD 11-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-SE002908.
XX
XX 29-DEC-2000; 2000SE-00004892.
XX
XX (PHAA ) PHARMACIA DIAGNOSTICS AB.
XX
XX Flicker S, Steinberger P, Kraft D, Valenta R;
XX
XX WPI; 2002-583604/62.
XX P-PSDB; ABG30447.
XX
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
XX variable region of group 2 allergen specific-human IgE Fabs, useful for
XX diagnosing or passive immunotherapy of type I allergy, for environmental
XX allergen detection.
XX
XX Disclosure; Page 33; 45pp; English.
XX
XX This invention relates to the DNA and protein sequences of group 2
XX allergen-specific human IgE Fabs and methods for their use. The proteins
XX of the invention may have antiallergic activities and may be used as a
XX vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
XX antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
XX 2 allergen-specific fabs of the invention may be useful for environmental
XX allergen detection and for standardisation of allergen extracts. The fabs
XX - or a vaccine against a type I allergy is useful for passive
XX immunotherapy of type I allergy, it is also useful for diagnosing a type
XX I allergy. The allergen-specific fabs of the invention are useful for
XX inter alia, diagnosis, therapy and prevention of type I allergy. They are
XX also useful for identification of group 2 allergen-containing pollen and
XX
XX Query Match 99.1%; Score 338.8; DB 6; Length 342;
XX Best Local Similarity 99.4%; Pred. No. 1.1e-85;
XX Matches 340; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 CTCGAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCTCTCCCTCACTGCCTGTC 60
XX
XX 1 CTCGAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCTCTCCCTCACTGCCTGTC 60
XX
XX 61 TCTGTGTGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGGATCGGCAGCGTCCAGGG 120
XX
XX 61 TCTGTGTGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGGATCGGCAGCGTCCAGGG 120
XX
XX 121 AAGGCCCTGGAGTGGATCGGTACATCTATCAGTGGCAACACCTACACACCGGTCC 180
XX
XX 121 AAGGCCCTGGAGTGGATCGGTACATCTATCAGTGGCAACACCTACACACCGGTCC 180
XX
XX 181 CTCAGAGTCGAGTTACCATGTCAGTACACAGTCTAAGAACCACTTCTCCCTGAGGCTG 240
XX
XX 181 CTCAGAGTCGAGTTACCATGTCAGTACACAGTCTAAGAACCACTTCTCCCTGAGGCTG 240
XX
XX 241 AGCTCTGTGACTGCGCGGACACCGCGGTGTTATTACTGTGCGAGGTTCAGATGGGTACACT 300
XX
XX 241 AGCTCTGTGACTGCGCGGACACCGCGGTGTTATTACTGTGCGAGGTTCAGATGGGTACACT 300
XX
XX 301 TTGGACAACTGGGCGGACCGGACCTGGTCAACCGTCTCTCA 342
XX
XX 301 TTGGACAACTGGGCGGACCGGACCGTGGTCAACCGTCTCTCA 342
XX
XX RESULT 2
XX ABK89638
XX ID ABK89638 standard; DNA; 342 BP.
XX
XX AC ABK89638;
```

XX DT 21-OCT-2002 (first entry)

XX DE DNA encoding human IgE Fab clone 60 heavy chain.

XX KW Human; fab; ds; gene; antiallergic; vaccine; grass pollen; Phi p 2;

XX KW timothy grass pollen allergen; passive immunotherapy.

XX OS Homo sapiens.

XX

XX Key Location/Qualifiers

XX FH 1..342

XX CDS /tag= a

XX /product= "Fab clone 60 heavy chain"

XX FT misc_feature 7..78

XX /tag= b

XX /note= "FR1 region"

XX FT misc_feature 79..99

XX /tag= c

XX /note= "CDR1 region"

XX FT misc_feature 100..123

XX /tag= d

XX /note= "FR2 region"

XX FT misc_feature 134..141

XX /tag= e

XX /note= "FR3 region"

XX FT misc_feature 142..189

XX /tag= f

XX /note= "CDR2 region"

XX FT misc_feature 190..285

XX /tag= g

XX /note= "FR3 region"

XX FT misc_feature 286..309

XX /tag= h

XX /note= "CDR3 region"

XX FT misc_feature 310..342

XX /tag= i

XX /note= "FR4 region"

XX

XX WO200253595-A1.

XX

XX 11-JUL-2002.

XX

XX 27-DEC-2001; 2001WO-SE002908.

XX

XX 29-DEC-2000; 2000SE-00004892.

XX (PHAA) PHARMACIA DIAGNOSTICS AB.

XX

XX Flicker S, Steinberger P, Kraft D, Valenta R;

XX

XX WPI; 2002-583604/62.

XX P-PSDB; ABG30446.

XX

XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising

XX variable region of group 2 allergen specific-human IgE Fabs, useful for

XX diagnosing or passive immunotherapy of type I allergy, for environmental

XX allergen detection.

XX

XX Disclosure; Page 32; 45pp; English.

XX

XX This invention relates to the DNA and protein sequences of group 2

XX allergen-specific human IgE Fabs and methods for their use. The proteins

XX of the invention may have antiallergic activities and may be used as a

XX vaccine or an inhibitor of binding of grass pollen allergic patient's IgE

XX antibodies to Phi p 2 (a major timothy grass pollen allergen). The group

XX 2 allergen-specific fabs of the invention may be useful for environmental

XX allergen detection and for standardisation of allergen extracts. The fabs

XX - or a vaccine against a type I allergy is useful for passive

XX immunotherapy of type I allergy, it is also useful for diagnosing a type

XX I allergy. The allergen-specific fabs of the invention are useful for

XX inter alia, diagnosis, therapy and prevention of type I allergy. They are

XX also useful for identification of group 2 allergen-containing pollen and

XX

CC may be used for blocking the binding of grass pollen allergic patients
 CC IGE antibodies to Phi p 2. The present sequence represents the DNA
 CC encoding the human IgG fab, clone 60 heavy chain protein of the invention
 XX
 SQ Sequence 342 BP; 70 A; 105 C; 90 G; 77 T; 0 U; 0 Other;

Query Match 94.4%; Score 322.8; DB 6; Length 342;
 Best Local Similarity 96.5%; Pred. No. 3.6e-81;
 Matches 330; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 QY 1 CTCGAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACCTGTC 60
 Db 1 CTCGAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACCTGTC 60
 QY 61 TCTGTGTGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGATCCGCCAGCTCCAGGG 120
 Db 61 TCTGTGTGCTCCATCCGAGTGGTGGTTATTATTGGAGTTGGTCCGCCAGCTCCAGGG 120
 QY 121 AAGGCCCTGGAGTGGATCGGTACATCTATCACAGTGGCAACCTACACACCCGTC 180
 Db 121 AAGGCCCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACCTACACACCCGTC 180
 QY 181 CTCAGAGTCTGAGTTACCATGTCTAGTACACAGCTCTAAGAACCACTTCTCCCTGAGGCTG 240
 Db 181 CTCAGAGTCTGAAATTACCATGTCTAGTACACAGCTCTAAGAACCACTTCTCCCTGAGACTG 240
 QY 241 AGCTCTGTGACTCGCGGACAGCGCCGTGTATTACTGTGGAGTCAAGTGGGTACACT 300
 Db 241 ACCTCTGTGACTCGCGGACAGCGCCGTCTATTACTGTGGCGGTCAAGTGGGTATACT 300
 QY 301 TTGGACAACCTGGGCCAGGAAACCTGTACCCGTCCTCA 342
 Db 301 TTGGACAACCTGGGCCAGGAAACCTGTACCCGTCCTCA 342

RESULT 3

ABK89637
 ID ABK89637 standard; DNA; 342 BP.

AC ABK89637;

DT 21-OCT-2002 (first entry)

DE DNA encoding human IgE Fab clone 94 heavy chain.

XX Human; fab; ds; gene; antiallergic; vaccine; grass pollen; Phi p 2;
 KW timothy grass pollen allergen; passive immunotherapy.

XX Homo sapiens.

PH Key Location/Qualifiers
 FT CDS 1..342
 FT /tag= a
 FT /product= "Fab clone 94 heavy chain"
 FT misc_feature 7..78
 FT /tag= b
 FT /note= "FR1 region"
 FT misc_feature 79..99
 FT /tag= c
 FT /note= "CDR1 region"
 FT misc_feature 100..123
 FT /tag= d
 FT /note= "FR2 region"
 FT misc_feature 134..141
 FT /tag= e
 FT /note= "FR3 region"
 FT misc_feature 142..189
 FT /tag= f
 FT /note= "CDR2 region"
 FT misc_feature 190..285
 FT /tag= g
 FT /note= "FR3 region"
 FT misc_feature 286..309

FT /tag= h
 FT /note= "CDR3 region"
 FT misc_feature 310..342
 FT /tag= i
 FT /note= "FR4 region"

XX WO200253595-A1.

PN 11-JUL-2002.

XX 27-DEC-2001; 2001WO-SE002908.

XX 29-DEC-2000; 2000SE-00004892.

XX (PHAA) PHARMACIA DIAGNOSTICS AB.

XX Flicker S, Steinberger P, Kraft D, Valenta R;

XX WPI; 2002-583604/62.

XX P-PSDB; ABG30445.

XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
 PT variable region of group 2 allergen specific-human IgE Fabs, useful for
 PT diagnosing or passive immunotherapy of type I allergy, for environmental
 PT allergen detection.

XX Disclosure; Page 31-32; 45pp; English.

XX This invention relates to the DNA and protein sequences of group 2
 CC allergen-specific human IgE Fabs and methods for their use. The proteins
 CC of the invention may have antiallergic activities and may be used as a
 CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
 CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
 CC 2 allergen-specific fabs of the invention may be useful for environmental
 CC allergen detection and for standardisation of allergen extracts. The fabs
 CC - or a vaccine against a type I allergy is useful for passive
 CC immunotherapy of type I allergy, it is also useful for diagnosing a type
 CC I allergy. The allergen-specific fabs of the invention are useful for
 CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
 CC also useful for identification of group 2 allergen-containing pollen and
 CC may be used for blocking the binding of grass pollen allergic patients
 CC IGE antibodies to Phi p 2. The present sequence represents the DNA
 CC encoding the human IgG fab, clone 94 heavy chain protein of the invention

XX Sequence 342 BP; 69 A; 100 C; 98 G; 75 T; 0 U; 0 Other;

Query Match 90.2%; Score 308.4; DB 6; Length 342;

Best Local Similarity 93.9%; Pred. No. 4.1e-77;

Matches 321; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 CTCGAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGTC 60
 Db 1 CTCGAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGTC 60
 QY 61 TCTGTGTGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGATCCGCCAGCTCCAGGG 120
 Db 61 TCTGTGTGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGATCCGCCAGCTCCAGGG 120
 QY 121 AAGGCCCTGGAGTGGATCGGGTACATCTATCACAGTGGCAACCTACACACCCGTC 180
 Db 121 AAGGCCCTGGAGTGGATCGGGTACATCTATCACAGTGGCAACCTACACACCCGTC 180
 QY 181 CTCAGAGTCTGAGTTACCATGTCTAGTACACAGCTCTAAGAACCACTTCTCCCTGAGGCTG 240
 Db 181 CTCAGAGTCTGAAATTGCCATGTCTAGTACACAGCTCTGAGAACCAAGTTCTCCCTGAGGCTG 240
 QY 241 AGCTCTGTGACTCGCGGACAGCGCCGTGTATTACTGTGGAGTCAAGTGGGTACACT 300
 Db 241 AACTCTGTGACTCGCGGACAGCGCCGTGTATTACTGTGGAGTGTAGTGGGTACACT 300
 QY 301 TTGGACAACCTGGGCCAGGAAACCTGTGTCACCCGTCCTCA 342
 Db 301 TTGGACAACCTGGGCCAGGAAACCTGTGTCACCCGTCCTCA 342

RESULT 4
ADC99786
ID ADC99786 standard; DNA; 352 BP.
XX
AC ADC99786;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-human MUC18 antibody heavy chain variable domain DNA SEQ ID 15.
XX
KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
XX cytotatic; melanoma; oesophageal; pancreatic; colorectal tumour;
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
XX lung cancer; human; ds; gene.
XX
OS Homo sapiens.
XX
PN WO2003057838-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041581.
XX
PR 28-DEC-2001; 2001US-0346299P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J;
XX
DR WPI; 2003-587113/55.
DR P-PSDB; ADC99784.
XX
XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease
PT or condition associated with expression of MUC18 in a patient, e.g.
PT tumors, cancers, and other malignancies.
XX
PS Claim 8; SEQ ID NO 15; 78pp; English.
XX
XX The invention relates to a novel isolated monoclonal antibody comprising
CC a heavy or light chain amino acid or a heavy or light chain variable
CC domain where the antibody binds to MUC18. The monoclonal antibody of the
CC invention demonstrates cytostatic activity and may be useful for treating
CC a disease or condition associated with the expression of MUC18 on the
CC cell surface such as tumours, specifically melanoma, oesophageal,
CC pancreatic or colorectal tumours, carcinomas, particularly cervical
CC carcinomas and cervical intraepithelial neoplasia and cancers including
CC colorectal, breast or lung cancer, as well as other malignancies. The
CC current sequence is that of the anti-human MUC18 monoclonal antibody
CC heavy chain variable domain DNA of the invention.
XX
SQ Sequence 352 BP; 73 A; 100 C; 103 G; 76 T; 0 U; 0 Other;

Query Match 83.2%; Score 284.6; DB 9; Length 352;
Best Local Similarity 92.0%; Pred. No. 2.1e-70;
Matches 312; Conservative 0; Mismatches 24; Indels 3; Gaps 1;

QY 4 GAGTCTGCCCGGAGCTGGTGAAGCCTTCACAGACCCTGCTCCCTCACCTGCACTGCTCT 63
DB 16 GAGTCTGCCCGGAGCTGGTGAAGCCTTCACAGACCCTGCTCCCTCACCTGCACTGCTCT 75

QY 64 GGTGGCTCCATCCGAGTGGTGGTATTACTGGAGTTGGATCCGCGAGCGTCCAGGGAAG 123
DB 76 GGTGGCTCCATCAGCAGTGGTGGTATTACTGGAGTTGGATCCGCGAGCAGCGGGAAG 135

QY 124 GGCCTGGAGTGGATCGGGTATCATCTATCATCAGTGGCAACACCTACAAACCCGCTCCCTC 183
DB 136 GGCCTGGAGTGGATCGGGTATCATCTATCATCAGTGGGAGCACCTACTACAAACCCGCTCCCTC 195

QY 184 AGAGTTCGAGTTACCATGTCAGTACAGTCTTAGAACCACTTCTCCCTGAGGCTGAGC 243
DB 196 AGAGTTCGAGTTACCATGTCAGTACAGTCTTAGAACCACTTCTCCCTGAGGCTGAGC 255

QY 244 TCTGTGACTGCCCGGACACCGCGCTGTATTACTGTGCGAGTCAAGTGGTACACTTGG 303
DB 256 TCTGTGACTGCCCGGACACCGCGCTGTATTACTGTGCGAG--AGAGGGAGATGGCTTT 312
QY 304 GACAACTGGGGCCAGGGAAACCTGTGTCACCGTCTCTCTCA 342
DB 313 GACTACTGGGGCCAGGGAAACCTGTGTCACCGTCTCTCTCA 351

RESULT 5
ADD05390
ID ADD05390 standard; DNA; 352 BP.
XX
AC ADD05390;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-MUC18 antibody heavy chain variable region DNA, SEQ ID No 15.
XX
KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
XX antigen; tumour metastasis; melanoma; metastatic; human; heavy chain;
XX gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003057006-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041582.
XX
PR 28-DEC-2001; 2001US-0346460P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J, Bar-Eli M;
XX
DR WPI; 2003-577496/54.
DR P-PSDB; ADD05388.
XX
XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT associated with melanoma, or increasing survival of an animal having a
PT metastatic tumor.
XX
PS Disclosure; SEQ ID NO 15; 87pp; English.
XX
XX The invention relates to a novel monoclonal antibody used for inhibiting
CC tumour growth in an animal. The tumour inhibition process comprises
CC selecting an animal in need of treatment for a tumour, providing a
CC monoclonal antibody comprising a heavy chain amino acid, where the
CC antibody consists of any one of 10 fully defined sequences of 117-123
CC amino acids given in the specification, and where the monoclonal antibody
CC binds MUC18, and contacting the tumour with the antibody resulting in
CC inhibited proliferation of the cells. The monoclonal antibody has
CC cytostatic and can be used in the production of a vaccine. The monoclonal
CC antibodies against the MUC18 antigen are useful for diagnosing and
CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
CC increasing survival of an animal having a metastatic tumour. This
CC polynucleotide sequence represents the DNA encoding an anti-MUC18
CC antibody heavy chain, variable region, protein of the invention.
XX
SQ Sequence 352 BP; 73 A; 100 C; 103 G; 76 T; 0 U; 0 Other;

Query Match 83.2%; Score 284.6; DB 9; Length 352;
Best Local Similarity 92.0%; Pred. No. 2.1e-70;
Matches 312; Conservative 0; Mismatches 24; Indels 3; Gaps 1;

QY 4 GAGTCTGCCCGGAGCTGGTGAAGCCTTCACAGACCCTGCTCCCTCACCTGCACTGCTCT 63
DB 16 GAGTCTGCCCGGAGCTGGTGAAGCCTTCACAGACCCTGCTCCCTCACCTGCACTGCTCT 75

QY 64 GGTGGCTCCATCCGACGTGGTGTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 123
 Db 76 GGTGGCTCCATCCGACGTGGTGTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 135
 QY 124 GGCCTGGAGTGGATCGGGTACATCTATCACAGTGGCAACCTACAACACCCCGTCCCTC 183
 Db 136 GGCCTGGAGTGGATCGGGTACATCTATCACAGTGGGAGCACCTACTACAACCCCGTCCCTC 195
 QY 184 AAGAGTCGAGTTACCATGTCTCAGTAGACACCGTCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
 Db 196 AAGAGTCGAGTTACCATGTCTCAGTAGACACCGTCTTAAGAACCACTTCTCCCTGAGGCTGAGC 255
 QY 244 TCTGTGACTCCGCGGACACGGCGGTGTATTACTGTGGAGTCCAGTGGGTACACTTTG 303
 Db 256 TCTGTGACTCCGCGGACACGGCGGTGTATTACTGTGGAGTCCAGTGGGTACACTTTG 312
 QY 304 GACAACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA 342
 Db 313 GACTACTGGGCGCAGGGAACCCCTGGTCACCGTCTCCTCA 351

RESULT 6

AA29076
 ID AAF29076 standard; DNA; 360 BP.

AC AAF29076;

XX 03-APR-2001 (first entry)

XX Human HIV-1 monoclonal antibody coding sequence SEQ ID NO: 32.

XX Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
 KW envelope glycoprotein; gp120; diagnosis; ds.

XX Homo sapiens.

XX WO200100678-A1.

XX 04-JAN-2001.

XX 23-JUN-2000; 2000WO-US017327.

XX 30-JUN-1999; 99US-0141701P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Watkins BA, Reitz MS;

XX WPI; 2001-112438/12.

DR P-PSDB; AAB62775.

XX Novel human monoclonal antibody immunoreactive with human
 PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
 PT in biological sample and providing passive immunotherapy to HIV-1
 PT infected mammal.

XX Claim 4; Page 45; 81pp; English.

XX The present invention provides the protein and coding sequences for the
 CC variable regions of human monoclonal antibodies which are immunoreactive
 CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
 CC These can be used in diagnosis and therapy of HIV-1 infection

XX Sequence 360 BP; 73 A; 104 C; 107 G; 76 T; 0 U; 0 Other;

Query Match 83.2%; Score 284.4; DB 4; Length 360;

Best Local Similarity 91.5%; Pred. No. 2.5e-70;

Matches 313; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

QY 4 GAGTCGCGCCAGGACTGGTGAAGCCTTACAGACACCGTGTCCCTCACCTGCACTGTCTCT 63

Db 19 GAGTCGCGCCAGGACTGGTGAAGCCTTACAGACACCGTGTCCCTCACCTGCACTGTCTCT 78

QY 64 GGTGGCTCCATCCGACGTGGTGTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 123
 Db 79 GGTGGCTCCATCCGACGTGGTGTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 138
 QY 124 GGCCTGGAGTGGATCGGGTACATCTATCACAGTGGCAACCTACAACACCCCGTCCCTC 183
 Db 139 GGCCTGGAGTGGATCGGGTACATCTATCACAGTGGGAGCACCTACTACAACCCCGTCCCTC 198
 QY 184 AAGAGTCGAGTTACCATGTCTCAGTAGACACCGTCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
 Db 199 AAGAGTCGAGTTACCATGTCTCAGTAGACACCGTCTTAAGAACCACTTCTCCCTGAGGCTGAGC 258
 QY 244 TCTGTGACTCCGCGGACACGGCGGTGTATTACTGTGGAGTCCAGTGGGTACACT 300
 Db 259 TCTGTGACTCCGCGGACACGGCGGTGTATTACTGTGGAGTCCAGTGGGTACACT 318
 QY 301 TTGGACAACCTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA 342
 Db 319 TTGGACCCTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA 360

RESULT 7

ADC99778

ID ADC99778 standard; DNA; 352 BP.

XX ADC99778;

XX 01-JAN-2004 (first entry)

XX Anti-human MUC18 antibody heavy chain variable domain DNA SEQ ID 7.

XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
 KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;
 KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
 KW lung cancer; human; ds; gene.

XX Homo sapiens.

XX WO2003057838-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041581.

XX 28-DEC-2001; 2001US-0346299P.

XX (ABGE-) ABGENIX INC.

XX Gudas J;

XX WPI; 2003-587113/55.

DR P-PSDB; ADC99776.

XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease
 PT or condition associated with expression of MUC18 in a patient, e.g.
 PT tumors, cancers, and other malignancies.

XX Claim 8; SEQ ID NO 7; 78pp; English.

XX The invention relates to a novel isolated monoclonal antibody comprising
 CC a heavy or light chain amino acid or a heavy or light chain variable
 CC domain where the antibody binds to MUC18. The monoclonal antibody of the
 CC invention demonstrates cytostatic activity and may be useful for treating
 CC a disease or condition associated with the expression of MUC18 on the
 CC cell surface such as tumours, specifically melanoma, oesophageal,
 CC pancreatic or colorectal tumours, carcinomas, particularly cervical
 CC carcinomas and cervical intraepithelial neoplasia and cancers including
 CC colorectal, breast or lung cancer, as well as other malignancies. The
 CC current sequence is that of the anti-human MUC18 monoclonal antibody
 CC heavy chain variable domain DNA of the invention.

XX Sequence 352 BP; 76 A; 102 C; 103 G; 71 T; 0 U; 0 Other;

Query Match 80.4%; Score 275; DB 9; Length 352;
Best Local Similarity 90.3%; Pred. No. 1.1e-67;
Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;
QY 4 GAGTTCGGCCAGGACTGGTGAAGCTTACAGACCCCTGTCCTACCTGCACTGTCTCT 63
DB 16 GAGTCGGGCCAGGACTGGTGAAGCTTACAGACCCCTGTCCTACCTGCACTGTCTCT 75
QY 64 GTGGCTCCATCGCAGTGGTGTATTACTGAGTTGGATCGCCAGCGTCCAGGGAAG 123
DB 76 GTGGCTCCATCAGCAGTGGTGTATTACTGAGTTGGATCGCCAGCGTCCAGGGAAG 135
QY 124 GGCCTGGAGTGGATCGGGTACATCTATCAGTGGCAACACCTTACAAACCCGTCCTC 183
DB 136 GGCCTGGAGTGGATCGGGTACATCTATCAGTGGGAGCACCTACTACACCCGTCCTC 195
QY 184 AAGAGTCGAGTTACCATGTCACTAGACAGCTCTAAGAACCACTTCTCCCTGAGGTGAGC 243
DB 196 AAGAGTCGAGTTACCATGTCACTAGACAGCTCTAAGAACCACTTCTCCCTGAGGTGAGC 255
QY 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGCGAGTTCAGATGGGTACACTTTG 303
DB 256 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGCGAGTTCAGATGGGTACACTTTG 312
QY 304 GACAACTGGGGCCAGGGAACCCCTGTCACCGTCTCTCTCA 342
DB 313 AAGTACTGGGGCCAGGGAACCCCTGTCACCGTCTCTCTCA 351

RESULT 8
ADD05382
ID ADD05382 standard; DNA; 352 BP.
XX
AC ADD05382;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-MUC18 antibody heavy chain variable region DNA, SEQ ID No 7.
XX
KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003057006-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041582.
XX
PR 28-DEC-2001; 2001US-0346460P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J, Bar-Eli M;
XX
DR WPI; 2003-577496/54.
DR P-PSDB; ADD05380.
XX

Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumor.

Disclosure; SEQ ID NO 7; 87pp; English.

The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123

CC amino acids given in the specification, and where the monoclonal antibody binds MUC18, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody has cytostatic and can be used in the production of a vaccine. The monoclonal antibodies against the MUC18 antigen are useful for diagnosing and treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or tumour metastasis), inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumour. This polynucleotide sequence represents the DNA encoding an anti-MUC18 antibody heavy chain, variable region, protein of the invention.

XX
SQ Sequence 352 BP; 76 A; 102 C; 103 G; 71 T; 0 U; 0 Other;
Query Match 80.4%; Score 275; DB 9; Length 352;
Best Local Similarity 90.3%; Pred. No. 1.1e-67;
Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;
QY 4 GAGTTCGGCCAGGACTGGTGAAGCTTACAGACCCCTGTCCTACCTGCACTGTCTCT 63
DB 16 GAGTCGGGCCAGGACTGGTGAAGCTTACAGACCCCTGTCCTACCTGCACTGTCTCT 75
QY 64 GTGGCTCCATCGCAGTGGTGTATTACTGAGTTGGATCGCCAGCGTCCAGGGAAG 123
DB 76 GTGGCTCCATCAGCAGTGGTGTATTACTGAGTTGGATCGCCAGCGTCCAGGGAAG 135
QY 124 GGCCTGGAGTGGATCGGGTACATCTATCAGTGGCAACACCTTACAAACCCGTCCTC 183
DB 136 GGCCTGGAGTGGATCGGGTACATCTATCAGTGGGAGCACCTACTACACCCGTCCTC 195
QY 184 AAGAGTCGAGTTACCATGTCACTAGACAGCTCTAAGAACCACTTCTCCCTGAGGTGAGC 243
DB 196 AAGAGTCGAGTTACCATGTCACTAGACAGCTCTAAGAACCACTTCTCCCTGAGGTGAGC 255
QY 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGCGAGTTCAGATGGGTACACTTTG 303
DB 256 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGCGAGTTCAGATGGGTACACTTTG 312
QY 304 GACAACTGGGGCCAGGGAACCCCTGTCACCGTCTCTCTCA 342
DB 313 AAGTACTGGGGCCAGGGAACCCCTGTCACCGTCTCTCTCA 351

RESULT 9
AAF29046
ID AAF29046 standard; DNA; 369 BP.
XX
AC AAF29046;
XX
DT 03-APR-2001 (first entry)
XX
DE Human HIV-1 monoclonal antibody coding sequence SEQ ID NO: 2.
XX
KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
KW envelope glycoprotein; gp120; diagnosis; ds.
XX
OS Homo sapiens.
XX
PN WO200100678-A1.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-US017327.
XX
PR 30-JUN-1999; 99US-0141701P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Watkins BA, Reitz MS;
XX
DR WPI; 2001-112438/12.
DR P-PSDB; AAB62745.
XX
PT Novel human monoclonal antibody immunoreactive with human

```
PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
PT in biological sample and providing passive immunotherapy to HIV-1
PT infected mammal.
XX
XX Claim 4; Page 34-35; 81pp; English.
XX
CC The present invention provides the protein and coding sequences for the
CC variable regions of human monoclonal antibodies which are immunoreactive
CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
CC These can be used in diagnosis and therapy of HIV-1 infection
XX
SQ Sequence 369 BP; 75 A; 104 C; 107 G; 83 T; 0 U; 0 Other;
Query Match 80.1%; Score 273.8; DB 4; Length 369;
Best Local Similarity 88.9%; Pred. No. 2.4e-67;
Matches 312; Conservative 0; Mismatches 27; Indels 12; Gaps 1;
QY 4 GAGTGTGCGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACTGTCTCT 63
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
19 GAGTCGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTTACCTGCACTGTCTCT 78
QY 64 GGTGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGGAATCCGCCAGCGTCCAGGGAAG 123
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
79 GGTGCTCCATCAGCAGTGGTGGTTACTACTGGAGTGGATCCGCCAGCACCCAGGGAAG 138
QY 124 GGCCTGGAGTGGATCGGGTACATCTATCACAGTGGCACTCAACAACCCGTCCTC 183
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
139 GGCCTGGAGTGGATGGGGTACATCTATTAACAGTGGGAGCCTCTACTAACCCTGTCCTC 198
QY 184 AAGAGTCGAGTTACCATGTCAGTAGACACGTCGTAAAGAACCACTTCTCCCTGAGGTGAGC 243
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
199 AAGAGTCGAGTTACCATATCAATAGACACGCTTAGAGACAGTTCTCCCTGAAGTGAAC 258
QY 244 TCTGTGACTGCGCGGACACGCGCGTGTTACTGTGCGAGTGC-----AGAT 291
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
259 TCTGTGACTGCGCGGACACGCGCGTGTTACTGTGCGAGGCGCGCGTATTGTGGTGGT 318
QY 292 GGGTACACTTTGGACAACCTGGGGCCAGGGAACCCCTGTCACCGTCTCCTCA 342
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
319 GATTGCTCCTTTGACTACTGGGGCCAGGGAACCCCTGGTGCACCGTCTCCTCA 369
RESULT 10
ADC99798
ID ADC99798 standard; DNA; 358 BP.
XX
XX AC ADC99798;
XX
XX DT 01-JAN-2004 (first entry)
XX
XX Anti-human MUC18 antibody heavy chain variable domain DNA SEQ ID 27.
XX
KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
KW cytosolic; melanoma; oesophageal; pancreatic; colorectal tumour;
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
KW lung cancer; human; ds; gene.
XX
XX Homo sapiens.
XX
XX WO2003057838-A2.
XX
XX 17-JUL-2003.
XX
XX 26-DEC-2002; 2002WO-US041581.
XX
XX 28-DEC-2001; 2001US-0346299P.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Gudas J;
XX
XX WPI; 2003-587113/55.
XX
XX P-PSDB; ADC99796.
XX
XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease
XX or condition associated with expression of MUC18 in a patient, e.g.
XX tumors, cancers, and other malignancies.
XX
XX Claim 8; SEQ ID NO 27; 78pp; English.
XX
CC The invention relates to a novel isolated monoclonal antibody comprising
CC a heavy or light chain amino acid or a heavy or light chain variable
CC domain where the antibody binds to MUC18. The monoclonal antibody of the
CC invention demonstrates cytostatic activity and may be useful for treating
CC a disease or condition associated with the expression of MUC18 on the
CC cell surface such as tumours, specifically melanoma, oesophageal,
CC pancreatic or colorectal tumours, carcinomas, particularly cervical
CC carcinomas and cervical intraepithelial neoplasia and cancers including
CC colorectal, breast or lung cancer, as well as other malignancies. The
CC current sequence is that of the anti-human MUC18 monoclonal antibody
CC heavy chain variable domain DNA of the invention.
XX
SQ Sequence 358 BP; 77 A; 103 C; 101 G; 77 T; 0 U; 0 Other;
Query Match 78.5%; Score 268.4; DB 9; Length 358;
Best Local Similarity 88.6%; Pred. No. 8e-66;
Matches 303; Conservative 0; Mismatches 36; Indels 3; Gaps 1;
QY 4 GAGTGTGCGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACTGTCTCT 63
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
16 GAGTCGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACTGTCTCT 75
QY 64 GGTGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGGAATCCGCCAGCGTCCAGGGAAG 123
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
76 GGTGCTCCATCAACAGTGGTGGTTGCTACTGGAGTGGATCCGCCAGCACCCAGGGAAG 135
QY 124 GGCCTGGAGTGGATCGGGTACATCTATCACAGTGGCACTCAACAACCCGTCCTC 183
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
136 GGCCTGGAGTGGATGGGTACATCTATTCCAGTGGGAGCACCTACTACAAACCCGTCCTC 195
QY 184 AAGAGTCGAGTTACCATGTCAGTAGACACGTCGTAAAGAACCACTTCTCCCTGAGGTGAGC 243
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
196 AAGAGTCGAGTTACCTTATCTATCAGTAGACACGTCGTAAAGAACCACTTCTCCCTGAAGCTGAAC 255
QY 244 TCTGTGACTGCGCGGACACGCGCGTGTTACTGTGCGAG---GTCAGATGGGTACACT 300
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
256 TCTATGACTGCGCGGACACGCGCGTGTTACTGTGCGAGAGATCGGGAACACAGCTGGT 315
QY 301 TTGGACAACCTGGGCGCAGGGAACCCCTGTCACCGTCTCCTCA 342
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
316 TTTGACTACTGGGCGCAGGGAACCCCTGGTGCACCGTCTCCTCA 357
RESULT 11
ADD05402
ID ADD05402 standard; DNA; 358 BP.
XX
XX AC ADD05402;
XX
XX DT 01-JAN-2004 (first entry)
XX
XX Anti-MUC18 antibody heavy chain variable region DNA, SEQ ID No 27.
XX
KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain;
KW gene; ds.
XX
XX Homo sapiens.
XX
XX WO2003057006-A2.
XX
XX 17-JUL-2003.
XX
XX 26-DEC-2002; 2002WO-US041582.
XX
XX 28-DEC-2001; 2001US-0346460P.
XX
```

XX (ABGE-) ABGENIX INC.
XX Gudas J, Bar-Eli M;
XX WPI; 2003-577496/54.
XX P-PSDB; ADD05400.
XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT associated with melanoma, or increasing survival of an animal having a
PT metastatic tumor.
XX
XX Disclosure; SEQ ID NO 27; 87pp; English.
XX
XX The invention relates to a novel monoclonal antibody used for inhibiting
CC tumour growth in an animal. The tumour inhibition process comprises
CC selecting an animal in need of treatment for a tumour, providing a
CC monoclonal antibody comprising a heavy chain amino acid, where the
CC antibody consists of any one of 10 fully defined sequences of 117-123
CC amino acids given in the specification, and where the monoclonal antibody
CC binds MUC18, and contacting the tumour with the antibody resulting in
CC inhibited proliferation of the cells. The monoclonal antibody has
CC cytostatic and can be used in the production of a vaccine. The monoclonal
CC antibodies against the MUC18 antigen are useful for diagnosing and
CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
CC increasing survival of an animal having a metastatic tumour. This
CC polynucleotide sequence represents the DNA encoding an anti-MUC18
CC antibody heavy chain, variable region, protein of the invention.
XX
SQ Sequence 358 BP; 77 A; 103 C; 101 G; 77 T; 0 U; 0 Other;

Query Match 78.5%; Score 268.4; DB 9; Length 358;
Best Local Similarity 88.6%; Pred. No. 8e-66;
Matches 303; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

QY 4 GAGTCGGCCCGAGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGCACCTGTCTCT 63
DB 16 GAGTCGGCCCGAGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGCACCTGTCTCT 75

QY 64 GGTGGCTCATCGCGAGTGGTGGTTATTAAGTGGAGTTGGATCGCGCAGCGTCCAGGGAAG 123
DB 76 GGTGGCTCATCAACAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 135

QY 124 GGCTCGAGTGGATGGGTACATCTATCACAGTGGCAACACCTACACAAACCGTCCCTC 183
DB 136 GGCTCGAGTGGATGGGTACATCTATTCAGTGGGAGCACCCTACTACAAACCGTCCCTC 195

QY 184 AAGAGTCGAGTTACCATGTCACTAGTACACGTCTAAGAACCACTTCTCCCTGAGGCTGAGC 243
DB 196 AAGAGTCGAGTTACCATGTCACTAGTACACGTCTAAGAACCACTTCTCCCTGAGGCTGAGC 255

QY 244 TCTGTGACTGCGCGGACAGCGCGGTGTTATTAAGTGGAGTGGAGTGGAGTGGAGTGGAGT 300
DB 256 TCTATGACTGCGCGGACAGCGCGGTGTTATTAAGTGGAGTGGAGTGGAGTGGAGTGGAGT 315

QY 301 TTGGCAACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342
DB 316 TTGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 357

RESULT 12
ID AAA46876
XX AAA46876 standard; DNA; 516 BP.
XX
AC AAA46876;
XX
XX 03-OCT-2000 (first entry)
XX
DE DNA encoding the heavy chain of immunoglobulin clone 2.1.1.3.
XX
KW Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;

KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
KW proliferative disorder; cancer; immunodeficient disorder; ss.
XX Homo sapiens.
XX WO200037504-A2.
XX 29-JUN-2000.
XX 23-DEC-1999; 99WO-US030895.
XX 23-DEC-1998; 98US-0113647P.
XX (PFIZ) PFIZER INC.
XX (ABGE-) ABGENIX INC.
XX Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
PI Corvalan JR;
XX WPI; 2000-442647/38.
XX P-PSDB; AAY93713.
XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)
PT -4 containing specified heavy and light chain sequences, useful for
PT treating, e.g. immune disorders.
XX
XX Example 2; Fig 1G; 157pp; English.
XX
XX The present sequence encodes a heavy chain of an antibody of the
CC invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)
CC -4. Antibodies of the invention are composed of a heavy chain variable
CC region, comprising a modified contiguous sequence from a FRI-FR3 sequence
CC encoded by a human VH3-33 family gene. The modifications are contained in
CC CDR1, CDR2 and/or framework regions. The antibodies may be used to
CC inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
CC disorders (e.g. autoimmune disease, diabetes and graft rejection) and
CC proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
CC used to up-regulate immune system to up-regulate immunodeficient
CC disorders.
XX
SQ Sequence 516 BP; 103 A; 167 C; 142 G; 104 T; 0 U; 0 Other;

Query Match 78.1%; Score 267.2; DB 3; Length 516;
Best Local Similarity 88.6%; Pred. No. 1.9e-65;
Matches 303; Conservative 0; Mismatches 33; Indels 6; Gaps 1;

QY 7 TCTGGCCCGAGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGCACCTGTCTCTGT 66
DB 1 TCGGGCCCGAGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGCACCTGTCTCTGT 60

QY 67 GGCTCCATCCGAGTGGTGGTTATTAAGTGGAGTTGGATCCGCGAGCGTCCAGGGAAGGC 126
DB 61 GGCTCCATCCGAGTGGTGGTTATTAAGTGGAGTTGGATCCGCGAGCGTCCAGGGAAGGC 120

QY 127 CTGGAGTGGATCGGTGATCATCTATCATAGTGGCAACCTACAAACCGTCCCTCAAG 186
DB 121 CTGGAGTGGATCGGTGATCATCTATCATAGTGGCAACCTACAAACCGTCCCTCAAG 180

QY 187 AGTCGAGTTACCATGTCACTAGTACACGTCTAGAACCACTTCTCCCTGAGGCTGAGCTCT 246
DB 181 AGTCGAGTTACCATGTCACTAGTACACGTCTAGAACCACTTCTCCCTGAGGCTGAGCTCT 240

QY 247 GTGACTGCGCGGACACCGCCGTGTATTACTGTGGAGTGCAGATGGG-----TACACT 300
DB 241 GTGACTGCGCGGACACCGCCGTGTATTATTGTGGAGAGATAGTGGGACTACTACGCT 300

QY 301 TTGGCAACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342
DB 301 ATAGACGTCTGGGGCCAGGGAACCCCGGTCAACCGTCTCTCTCA 342

RESULT 13
AAF29066

```

ID AAF29066 standard; DNA; 366 BP.
XX
AC AAF29066;
XX
XX 03-APR-2001 (first entry)
XX
XX Human HIV-1 monoclonal antibody coding sequence SEQ ID NO: 22.
XX
XX Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
XX envelope glycoprotein; gp120; diagnosis; ds.
XX
XX Homo sapiens.
XX
XX WO200100678-A1.
XX
XX 04-JAN-2001.
XX
XX 23-JUN-2000; 2000WO-US017327.
XX
XX 30-JUN-1999; 99US-0141701P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Watkins BA, Reitz MS;
XX
XX WPI; 2001-112438/12.
XX
XX P-PSDB; AAB62765.
XX
XX Novel human monoclonal antibody immunoreactive with human
XX immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
XX in biological sample and providing passive immunotherapy to HIV-1
XX infected mammal.
XX
XX Claim 4; Page 42; 81pp; English.
XX
XX The present invention provides the protein and coding sequences for the
XX variable regions of human monoclonal antibodies which are immunoreactive
XX with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
XX These can be used in diagnosis and therapy of HIV-1 infection
XX
XX Sequence 366 BP; 73 A; 107 C; 106 G; 80 T; 0 U; 0 Other;
XX
XX Query Match 77.2%; Score 264; DB 4; Length 366;
XX Best Local Similarity 87.4%; Pred. No. 1.4e-64;
XX Matches 304; Conservative 0; Mismatches 35; Indels 9; Gaps 1;
QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCTGTCCCTCACCTGCACCTGTCTCT 63
Db 19 GAGTGGGGCCAGGACTGGTGAAGCCTTCACAGACCTGTCCCTCACCTGCACCTGTCTCT 78
QY 64 GGTGGCTCCATCCGACGTGGTGTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 123
Db 79 GGTGGCTCCATCCGACGTGGTGTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 138
QY 124 GGCTTGAGTGGATCGGGTACATCTATCAGTGGGCAACACCTACAAACACCGTCCCTC 183
Db 139 GGCTTGAGTGGATCGGGTACATCTATCAGTGGGAGACCTACTACACCCGTCCTC 198
QY 184 AAGAGTCAGATTACCATGTTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGCTGAGC 243
Db 199 AAGAGTCAGATTACCATGTTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGCTGAGC 258
QY 244 TCTGTGACTGCGGGACAGCGCGGTGTATTACTGTGCGAGGACATGCTACGGGACTCT 294
Db 259 TCTGTGACTGCGGGACAGCGCGGTGTATTACTGTGCGAGGACATGCTACGGGACTCT 318
QY 295 TACACTTTGGACAACTGGGGCCAGGGAAACCTGGTCAACCGTCTCTCTCA 342
Db 319 ACTGGACTGTCTACTGGGGCCGTGGCAACCTGGTCAACCGTCTCTCTCA 366

ID AAQ38670 standard; cDNA; 357 BP.
XX
XX AAQ38670;
XX
XX 25-MAR-2003 (revised)
XX
XX 06-MAY-1993 (first entry)
XX
XX MAb GAH variable region of heavy chain.
XX
XX Monoclonal antibody; hybridoma; PCR; variable region; constant region;
XX heavy chain; light chain; ss.
XX
XX Synthetic.
XX
XX EP520499-A1.
XX
XX 30-DEC-1992.
XX
XX 26-JUN-1992; 92EP-00110841.
XX
XX 28-JUN-1991; 91JP-00158859.
XX
XX 28-JUN-1991; 91JP-00158860.
XX
XX 28-JUN-1991; 91JP-00158861.
XX
XX (MITU ) MITSUBISHI KASEI CORP.
XX
XX Hosokawa S, Tagawa T, Hirakawa Y, Ito N, Nagaike K;
XX
XX WPI; 1993-001328/01.
XX
XX P-PSDB; AAR30143.
XX
XX Human monoclonal antibody specific for a cancer cell membrane surface
XX antigen - prepd. from a hybridoma obtd. by cell fusion between human
XX lymphocytes derived from cancer patients and mouse myeloma cells.
XX
XX Claim 13; Page 31 + 14-15; 37pp; English.
XX
XX A human MAb specifically binding to a surface antigen of cancer cell
XX membrane comprises variable regions of the heavy and light chains having
XX the amino acid sequences of AAR30143-44 respectively, encoded by DNA
XX sequences AAQ38670 and AAQ33032 respectively. (Updated on 25-MAR-2003 to
XX correct PN field.)
XX
XX Sequence 357 BP; 73 A; 105 C; 102 G; 77 T; 0 U; 0 Other;
XX
XX Query Match 77.1%; Score 263.6; DB 2; Length 357;
XX Best Local Similarity 87.7%; Pred. No. 1.8e-64;
XX Matches 300; Conservative 0; Mismatches 39; Indels 3; Gaps 1;
QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCTGTCCCTCACCTGCACCTGTCTCT 63
Db 16 GAGTGGGGCCAGGACTGGTGAAGCCTTCACAGACCTGTCCCTCACCTGCACCTGTCTCT 75
QY 64 GGTGGCTCCATCCGACGTGGTGTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 123
Db 76 GGTGGCTCCATCCGACGTGGTGTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 135
QY 124 GGCTTGAGTGGATCGGGTACATCTATCAGTGGGCAACACCTACAAACACCGTCCCTC 183
Db 136 GGCTTGAGTGGATCGGGTACATCTATCAGTGGGAGCACCTACTACAAACCGTCCCTC 195
QY 184 AAGAGTCAGATTACCATGTTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGCTGAGC 243
Db 196 AAGAGTCAGATTACCATGTTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGCTGAGC 255
QY 244 TCTGTGACTGCGGGACAGCGCGGTGTATTACTGTGCGAGGTCAGATGGGTACACTTTG 303
Db 256 TCTGTGACTGCGGGACAGCGCGGTGTATTACTGTGCGAGGTCAGATGGGTACACTTTG 315
QY 304 ---GACAACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342
Db 316 GCTGACTACTGGGGCCAGGGAACAAATGGTCAACCGTCTCTCTCA 357

RESULT 14
AAQ38670

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OM nucleic - nucleic search, using sw model

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2207.472 Million cell updates/sec

Title: US-10-027-725A-3

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Scoring table: IDENTITY NUC

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	310	90.6	342	15	US-10-027-725A-2
4	284.6	83.2	352	15	US-10-330-613-15
5	284.6	83.2	352	15	US-10-330-613-15
6	284.6	83.2	352	17	US-10-330-613-15
7	275.8	80.6	663	10	US-09-972-656-79
8	275	80.4	352	15	US-10-330-613-7
9	275	80.4	352	15	US-10-330-613-7
10	275	80.4	352	17	US-10-660-357-7
11	270.8	79.2	370	16	US-10-309-762-186
12	268.4	78.5	358	15	US-10-330-613-27
13	268.4	78.5	358	15	US-10-330-613-27
14	268.4	78.5	358	17	US-10-660-357-27

15	267.8	78.3	429	16	US-10-309-762-110	Sequence 110, App
16	267.6	78.2	370	16	US-10-309-762-189	Sequence 189, App
17	267	78.1	361	16	US-10-309-762-191	Sequence 191, App
18	265	77.5	370	16	US-10-309-762-185	Sequence 185, App
19	264.2	77.3	367	16	US-10-309-762-195	Sequence 195, App
20	262.8	76.8	352	15	US-10-330-613-35	Sequence 35, Appl
21	262.8	76.8	352	15	US-10-330-613-35	Sequence 35, Appl
22	262.8	76.8	352	17	US-10-660-357-35	Sequence 35, Appl
23	261.6	76.5	376	16	US-10-309-762-184	Sequence 184, App
24	261.6	76.5	376	16	US-10-309-762-197	Sequence 197, App
25	261.6	76.5	376	16	US-10-309-762-199	Sequence 199, App
26	261.2	76.4	370	16	US-10-309-762-200	Sequence 200, App
27	260.6	76.2	352	16	US-10-309-762-203	Sequence 203, App
28	260	76.0	376	16	US-10-309-762-187	Sequence 187, App
29	259.6	75.9	519	16	US-10-309-762-174	Sequence 174, App
30	258.6	75.6	382	16	US-10-309-762-194	Sequence 194, App
31	257.4	75.3	361	16	US-10-309-762-193	Sequence 193, App
32	257	75.1	324	9	US-09-864-761-31244	Sequence 31244, A
33	256.4	75.0	370	16	US-10-309-762-201	Sequence 201, App
34	256.4	75.0	370	16	US-10-309-762-212	Sequence 212, App
35	255.8	74.8	450	15	US-10-390-986-13	Sequence 13, Appl
36	253.8	74.2	381	17	US-10-312-316-66	Sequence 66, Appl
37	253.8	74.2	384	17	US-10-312-316-68	Sequence 68, Appl
38	250.6	73.3	381	17	US-10-312-316-64	Sequence 64, Appl
39	248.8	72.7	378	9	US-09-974-449-5	Sequence 5, Appl
40	248.4	72.6	393	9	US-09-925-299-198	Sequence 198, App
41	248.4	72.6	393	10	US-09-925-299-198	Sequence 198, App
42	245.8	71.9	1543	9	US-09-800-729-74	Sequence 74, Appl
43	243.4	71.2	349	12	US-10-269-711-2	Sequence 2, Appl
44	242.4	70.9	417	9	US-09-905-243-7	Sequence 7, Appl
45	240	70.2	462	17	US-10-693-629-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1

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US-10-027-725A-3
; Sequence 3, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-027-725A-3
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Best Local Similarity		100.0%;	Pred. No. 1.4e-102;		
Matches 342;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	CTCGAGTGTGCCCAGGACTGGTGAAGCTTTCAGACACCCCTGTCCTCACCTGACCTGTC	60		
Db	1	CTCGAGTGTGCCCAGGACTGGTGAAGCTTTCAGACACCCCTGTCCTCACCTGACCTGTC	60		
Qy	61	TCTGTTGGTCCATCCCGCAGTGGTGGTTATTACTGGAGTTGGATCCGCGCAGCTCCAGGG	120		
Db	61	TCTGTTGGTCCATCCCGCAGTGGTGGTTATTACTGGAGTTGGATCCGCGCAGCTCCAGGG	120		
Qy	121	AAGGCTTGGAGTGGATCGGGTACATCTATCAGAGTGGCAACACCTACCAACACCCGTC	180		
Db	121	AAGGCTTGGAGTGGATCGGGTACATCTATCAGAGTGGCAACACCTACCAACACCCGTC	180		
Qy	181	CTCAGAGTCCAGTTACCATCTAGTACAGACGCTTAAGAACCACTTCTCCCTGAGGGTG	240		

Db 181 CTCAGAGTCGAGTTACCATGTTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTG 240
QY 241 AGCTCTGTGACTGCCGCGACACGCGGTGTTACTGTGCGAGTTCAGATGGGTACACT 300
Db 241 AGCTCTGTGACTGCCGCGACACGCGGTGTTACTGTGCGAGTTCAGATGGGTACACT 300
QY 301 TTGGACAACTGGGGCCAGGGAACCCCTGGTCAACGCTCTCTCTCA 342
Db 301 TTGGACAACTGGGGCCAGGGAACCCCTGGTCAACGCTCTCTCTCA 342

RESULT 2

US-10-027-725A-2
; Sequence 2, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; PRIOR APPLICATION NUMBER: 2002-08-09
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-027-725A-2

Query Match 94.9%; Score 324.4; DB 15; Length 342;
Best Local Similarity 96.8%; Pred. No. 9.3e-97;
Matches 331; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 CTCGAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACTGCACTGTC 60
Db 1 CTCGAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACTGCACTGTC 60
QY 61 TCTGTGGCTCCATCCGAGTGGTGGTTACTGTGAGTGGATCGGCGAGGTCAGGG 120
Db 61 TCTGTGGCTCCATCCGAGTGGTGGTTACTGTGAGTGGATCGGCGAGGTCAGGG 120
QY 121 AAGGCCCTGGAGTGGATCGGTACATCTATCACAGTGGCAACACCTACAACACCCGTC 180
Db 121 AAGGCCCTGGAGTGGATCGGTACATCTATCACAGTGGCAACACCTACAACACCCGTC 180
QY 181 CTCAGAGTCGAGTTACCATGTTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTG 240
Db 181 CTCAGAGTCGAAATTCACATGTTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTG 240
QY 241 AGCTCTGTGACTGCCGCGACACGCGGTGTTACTGTGCGAGTTCAGATGGGTACACT 300
Db 241 ACCTCTGTGACTGCCGCGACACGCGGTGTTACTGTGCGAGTTCAGATGGGTACACT 300
QY 301 TTGGACAACTGGGGCCAGGGAACCCCTGGTCAACGCTCTCTCTCA 342
Db 301 TTGGACAACTGGGGCCAGGGAACCCCTGGTCAACGCTCTCTCTCA 342

RESULT 3

US-10-027-725A-1
; Sequence 1, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; PRIOR APPLICATION NUMBER: 2002-08-09
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2000-12-29

; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-027-725A-1

Query Match 90.6%; Score 310; DB 15; Length 342;
Best Local Similarity 94.2%; Pred. No. 5.3e-92;
Matches 322; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 CTCGAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACTGCACTGTC 60
Db 1 CTCGAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACTGCACTGTC 60
QY 61 TCTGTGGCTCCATCCGAGTGGTGGTTACTGTGAGTGGATCGGCGAGGTCAGGG 120
Db 61 TCTGTGGCTCCATCCGAGTGGTGGTTACTGTGAGTGGATCGGCGAGGTCAGGG 120
QY 121 AAGGCCCTGGAGTGGATCGGTACATCTATCACAGTGGCAACACCTACAACACCCGTC 180
Db 121 AAGGCCCTGGAGTGGATCGGTACATCTATCACAGTGGCAACACCTACAACACCCGTC 180
QY 181 CTCAGAGTCGAGTTACCATGTTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTG 240
Db 181 CTCAGAGTCGAAATTCACATGTTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTG 240
QY 241 AGCTCTGTGACTGCCGCGACACGCGGTGTTACTGTGCGAGTTCAGATGGGTACACT 300
Db 241 AACTCTGTGACTGCCGCGACACGCGGTGTTACTGTGCGAGTTCAGATGGGTACACT 300
QY 301 TTGGACAACTGGGGCCAGGGAACCCCTGGTCAACGCTCTCTCTCA 342
Db 301 TTGGACAACTGGGGCCAGGGAACCCCTGGTCAACGCTCTCTCTCA 342

RESULT 4

US-10-330-613-15
; Sequence 15, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-613-15

Query Match 83.2%; Score 284.6; DB 15; Length 352;
Best Local Similarity 92.0%; Pred. No. 1.3e-83;
Matches 312; Conservative 0; Mismatches 24; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACTGCACTGTCCT 63
Db 16 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACTGCACTGTCCT 75
QY 64 GGTGGCTCCATCCGAGTGGTGGTTACTGTGAGTGGATCGGCGAGGTCAGGGAG 123
Db 76 GGTGGCTCCATCCGAGTGGTGGTTACTGTGAGTGGATCGGCGAGGTCAGGGAG 135
QY 124 GGCCTGGAGTGGATCGGCTACATCTATCACAGTGGCAACACCTACAACACCCGTCCTC 183
Db 136 GGCCTGGAGTGGATCGGCTTCTATCTATTACAGTGGGAGCACTACTACAACCCGTCCTC 195

Db 76 GGTGGCTCCATCAGCAGTGGTGTACTCTCTGGAGCTGGATCCGGCAGCCACCAGGGAAG 135
QY 124 GGCTTGGAGTGGATCGGTACATCTATCAGTGGCAACACCTTACAAACCCGTCCTC 183
Db 136 GGCTTGGAGTGGATCGGTACATCTATCAGTGGGAGCACCTTACAAACCCGTCCTC 195
QY 184 AAGAGTCGAGTTACCATGTCTAGTAGACAGTCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db 196 AAGAGTCGAGTCAACATATCAGTAGACAGTCTCAAGAACCACTTCTCCCTGAGGCTGAGC 255
QY 244 TCTGTGACTGCGCGGACACGGCGGTATTACTGTGCGAGTCAGATGGGTACACTTTG 303
Db 256 TCTGTGACTGCGCGGACACGGCGGTATTACTGTGCGAGTCAGATGGGTACACTTTG 303
QY 304 GACAACTGGGGCCAGGGAACCTTGGTCAACCGTCTC 338
Db 316 GACTACTGGGGCCAGGGAACCTTGGTCAACCGTCTC 350

RESULT 8

US-10-330-613-7
; Sequence 7, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-613-7

Query Match 80.4%; Score 275; DB 15; Length 352;
Best Local Similarity 90.3%; Pred. No. 1.9e-80;
Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTACAGACCCCTGTCCCTCACCTGCACTGTCTCT 63
Db 16 GAGTCTGGCCAGGACTGGTGAAGCCTTACAGACCCCTGTCCCTCACCTGCACTGTCTCT 75
QY 64 GGTGCTCCATCCGAGTGGTGTATTACTGGAGTTGGATCCGCGCAGCGTCCAGGGAAG 123
Db 76 GGTGCTCCATCCGAGTGGTGTATTACTGGAGTTGGATCCGCGCAGCGTCCAGGGAAG 135
QY 124 GGCTTGGAGTGGATCGGTACATCTATCAGTGGCAACACCTTACAAACCCGTCCTC 183
Db 136 GGCTTGGAGTGGATCGGTACATCTATCAGTGGGAGCACCTTACAAACCCGTCCTC 195
QY 184 AAGAGTCGAGTTACCATGTCTAGTAGACAGTCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db 196 AAGAGTCGAGTCAACATATCAGTAGACAGTCTCAAGAACCACTTCTCCCTGAGGCTGAGC 255
QY 244 TCTGTGACTGCGCGGACACGGCGGTATTACTGTGCGAGTCAGATGGGTACACTTTG 303
Db 256 TCTGTGACTGCGCGGACACGGCGGTATTACTGTGCGAGTCAGATGGGTACACTTTG 303
QY 304 GACAACTGGGGCCAGGGAACCTTGGTCAACCGTCTCTCTCA 342
Db 313 AAGTACTGGGGCCAGGGAACCTTGGTCAACCGTCTCTCTCA 351

RESULT 9

US-10-330-530-7
; Sequence 7, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:

; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-530-7

Query Match 80.4%; Score 275; DB 15; Length 352;
Best Local Similarity 90.3%; Pred. No. 1.9e-80;
Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;
QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTACAGACCCCTGTCCCTCACCTGCACTGTCTCT 63
Db 16 GAGTCTGGCCAGGACTGGTGAAGCCTTACAGACCCCTGTCCCTCACCTGCACTGTCTCT 75
QY 64 GGTGCTCCATCCGAGTGGTGTATTACTGGAGTTGGATCCGCGCAGCGTCCAGGGAAG 123
Db 76 GGTGCTCCATCCGAGTGGTGTATTACTGGAGTTGGATCCGCGCAGCGTCCAGGGAAG 135
QY 124 GGCTTGGAGTGGATCGGTACATCTATCAGTGGGAGCACCTTACAAACCCGTCCTC 183
Db 136 GGCTTGGAGTGGATCGGTACATCTATCAGTGGGAGCACCTTACAAACCCGTCCTC 195
QY 184 AAGAGTCGAGTTACCATGTCTAGTAGACAGTCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db 196 AAGAGTCGAGTCAACATATCAGTAGACAGTCTTAAGAACCACTTCTCCCTGAGGCTGAGC 255
QY 244 TCTGTGACTGCGCGGACACGGCGGTGTATTACTGTGCGAGTCAGATGGGTACACTTTG 303
Db 256 TCTGTGACTGCGCGGACACGGCGGTGTATTACTGTGCGAGTCAGATGGGTACACTTTG 303
QY 304 GACAACTGGGGCCAGGGAACCTTGGTCAACCGTCTCTCTCA 342
Db 313 AAGTACTGGGGCCAGGGAACCTTGGTCAACCGTCTCTCTCA 351

RESULT 10

US-10-660-357-7
; Sequence 7, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-660-357-7

Query Match 80.4%; Score 275; DB 17; Length 352;
Best Local Similarity 90.3%; Pred. No. 1.9e-80;
Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTACAGACCCCTGTCCCTCACCTGCACTGTCTCT 63
Db 16 GAGTCTGGCCAGGACTGGTGAAGCCTTACAGACCCCTGTCCCTCACCTGCACTGTCTCT 75

Qy 64 GGTGGCTCCATCCGACGTGGTGTATTACTGGAGTTGGATCGCCAGCGTCCAGGGAAG 123
Db 76 GGTGGCTCCATCCGACGTGGTGTATTACTGGAGTTGGATCGCCAGCGTCCAGGGAAG 135
Qy 124 GGCTGGAGTGGATCGGGTACATCTATCAGAGTGGCAACCTTACAAACACCCGTCCTC 183
Db 136 GGCTGGAGTGGATCGGGTACATCTATCAGAGTGGCAACCTTACAAACACCCGTCCTC 195
Qy 184 AAGAGTCGAGTTACCATGTTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db 196 AAGAGTCGAGTTACCATGTTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 255
Qy 244 TCTGTGACTCCGCGGACACGGCCGTGTATTACTGTGCGAGTCAGATGGGTACACTTTG 303
Db 256 TCTGTGACTCCGCGGACACGGCCGTGTATTACTGTGCGAGTCAGATGGGTACACTTTG 312
Qy 304 GACAACTGGGCGCAGGGAACCTGTTCACCGTCTCTCTCA 342
Db 313 AAGTACTGGGCGCAGGGAACCTGTTCACCGTCTCTCTCA 351

RESULT 11

US-10-309-762-186
; Sequence 186, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXY ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 186
; LENGTH: 370
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-309-762-186

Query Match 79.2%; Score 270.8; DB 16; Length 370;
Best Local Similarity 88.1%; Pred. No. 4.6e-79;
Matches 312; Conservative 0; Mismatches 27; Indels 15; Gaps 1;
Qy 4 GAGTCTGGCCGAGGACTGGTGAAGCCTTACAGACCCCTGTCCCTCAGCTGCTCT 63
Db 16 GAGTCGGGCCGAGGACTGGTGAAGCCTTACAGACCCCTGTCCCTCAGCTGCTCT 75
Qy 64 GGTGGCTCCATCCGACGTGGTGTATTACTGGAGTTGGATCGCCAGCGTCCAGGGAAG 123
Db 76 GGTGGCTCCATCCGACGTGGTGTATTACTGGAGTTGGATCGCCAGCACCCAGGGAAG 135
Qy 124 GGCTGGAGTGGATCGGGTACATCTATCAGAGTGGCAACCTTACAAACACCCGTCCTC 183
Db 136 GGCTGGAGTGGATCGGGTACATCTATCAGAGTGGGAGCACTTACTAAACCCGTCCTC 195
Qy 184 AAGAGTCGAGTTACCATGTTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db 196 AAGAGTCGAGTTACCATGTTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 255
Qy 244 TCTGTGACTCCGCGGACACGGCCGTGTATTACTGTGCGAGTCAGATGGGTACACT--- 300
Db 256 TCTGTGACTCCGCGGACACGGCCGTGTATTACTGTGCGAGTCAGATGGGTATATGGT 315
Qy 301 -----TTGGACAACTGGGGCCAGGGAACCCCTGGTCACCGTCTCTCTCA 342
Db 316 TCGGGGAGTTACCTTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCTCTCA 369

RESULT 12

US-10-330-613-27
; Sequence 27, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-613-27

Query Match 78.5%; Score 268.4; DB 15; Length 358;
Best Local Similarity 88.6%; Pred. No. 2.9e-78;
Matches 303; Conservative 0; Mismatches 36; Indels 3; Gaps 1;
Qy 4 GAGTCTGGCCGAGGACTGGTGAAGCCTTACAGACCCCTGTCCCTCAGCTGCTCT 63
Db 16 GAGTCGGGCCGAGGACTGGTGAAGCCTTACAGACCCCTGTCCCTCAGCTGCTCT 75
Qy 64 GGTGGCTCCATCCGACGTGGTGTATTACTGGAGTTGGATCGCCAGCGTCCAGGGAAG 123
Db 76 GGTGGCTCCATCCGACGTGGTGTATTACTGGAGTTGGATCGCCAGCACCCAGGGAAG 135
Qy 124 GGCTGGAGTGGATCGGGTACATCTATCAGAGTGGCAACCTTACAAACACCCGTCCTC 183
Db 136 GGCTGGAGTGGATCGGGTACATCTATCAGAGTGGGAGCACCTTACTAAACCCGTCCTC 195
Qy 184 AAGAGTCGAGTTACCATGTTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db 196 AAGAGTCGAAATTACCTTATCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAAC 255
Qy 244 TCTGTGACTCCGCGGACACGGCCGTGTATTACTGTGCGAGTCAGATGGGTACACT 300
Db 256 TCTATGACTCGCGGAGACAGCGCGTGTATTACTGTGCGAGATCGGGAACAGCTGGT 315
Qy 301 TTGGACAACTGGGCGCAGGGAACCCCTGGTCACCGTCTCTCTCA 342
Db 316 TTTGACTACTGGGCGCAGGGAACCCCTGGTCACCGTCTCTCTCA 357

RESULT 13

US-10-330-530-27
; Sequence 27, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-530-27

Query Match 78.5%; Score 268.4; DB 15; Length 358;
Best Local Similarity 88.6%; Pred. No. 2.9e-78;

Matches	303;	Conservative	0;	Mismatches	36;	Indels	3;	Gaps	1;
Qy	4	GAGTCTGGCCGAGAC	TGGTGAAGCC	TTCA	CAGACCC	TGTCCCT	TCACTGAC	TGCTCTCT	63
Db	16	GAGTCGGGGCCGAGAC	TGGTGAAGCC	TTCA	CAGACCC	TGTCCCT	TCACTGAC	TGCTCTCT	75
Qy	64	GGTGGCTCCAT	TCGCGACGTGGTGGT	TTA	TACTGGAG	TTGGATCG	CGCCAGCC	TC	123
Db	76	GGTGGCTCCAT	CAACAGTGGTGGT	TTGCTACT	GGAGCTGGAT	TCGCGCAG	CA	CCCGGAAG	135
Qy	124	GGCCTGAGATGGAT	TCGGGTACAT	CTAT	TCA	CAGTGGGCAAC	CTTACAA	CA	183
Db	136	GGCCTGAGATGGAT	TGGGTACAT	CTAT	TCCAGTGGGAG	CACTACTACA	CA	CCCGTCCCTC	195
Qy	184	AAGAGTCGAGT	TACCATGT	CAGTAGACAC	GTCTAAGAA	CACTTCTCCCT	TGAGGCTGAC	C	243
Db	196	AAGAGTCGAT	TACCTTAT	CAGTAGACAC	GTCTAAGAA	CACTTCTCCCT	TGAGGCTGAC	C	255
Qy	244	TCTGTGACT	GC	CGCGGACAG	CGCCG	TGTATTACT	TGTCGAG	--	300
Db	256	TCTATGACT	GC	CGCGGACAG	CGCCG	TGTATTACT	TGTCGAGAGAT	CGG	315
Qy	301	TTTGACAAC	TGGGGCCAGGGAA	CCCTGGT	CACCGT	CTCCTCA			342
Db	316	TTTGACT	TA	CTGGGGCCAGGGAA	CCCTGGT	CACCGT	CTCCTCA		357

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RESULT 14
US-10-660-357-27
; Sequence 27, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ANTIGEN
; FILE REFERENCE: ARGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-660-357-27

Query Match          78.5%; Score 268.4; DB 17; Length 358;
Best Local Similarity 88.6%; Pred. No. 2.9e-78;
Matches 303; Conservative 0; Mismatches 36; Indels 3; Gaps 1

QY 4 GAGTCTGGCCGACGACTGGTGAAGCCCTTCACAGACCCCTGTCCTCACTGCACCTGCTCTCT 63
Db 16 GAGTCGGGGCCGAGACTGGTGAAGCCCTTCACAGACCCCTGTCCTCACTGCACCTGCTCTCT 75
QY 64 GGTGGCTCCATCCGACGTGGTGGTATTACTGGAGTTGGATCCGGCCAGCGTCCAGGGGAG 123
Db 76 GGTGGCTCCATCAACACGTGGTGGTGGTACTGGAGCTGGATCCGCCAGCACCCAGGGGAG 135
QY 124 GGCTGTGAGTGGATCGGGTACATCTATCAAGTGGCAACACTACAAACACCGGCCCTC 183
Db 136 GGCTGTGAGTGGATCGGGTACATCTATTCAGTGGGACGACTACTACAACCGCGTCCCTC 195
QY 184 AAGAGTCCGAGTTACCATGTCACTAGACACACGCTTAAGAACCACTTCTCCCTCAGGCTGAGC 243
Db 196 AAGAGTCCGATTACTTATCACTAGTACACAGCTTAAGAACCACTTCTCCCTGAAGCTGAAC 255
QY 244 TCTGTGACTGCGCGGACACGCGCGTGATTACTGTGGAG--GTCAGATGGGTACACT 300
Db 256 TCTATGACTGCGCGGACACGCGCGTGATTACTGTGGAGAGATCGGGAAACAGCTGCT 315

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Qy	301	TTGACAACTGGGCCACGGGAACCCCTGGTCACCGTCTCTCA	342
Db	316	TTTGACTACTGGGCCACGGGAACCCCTGGTCACCGTCTCTCA	357
RESULT 15			
US-10-309-762-110			
; Sequence 110, Application US/10309762			
; Publication No. US20040018198A1			
; GENERAL INFORMATION:			
; APPLICANT: Gudas, Jean			
; APPLICANT: Foltz, Ian			
; APPLICANT: Handa, Masahisa			
; APPLICANT: Gallo, Michael			
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX			
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN			
; FILE REFERENCE: AGENIX.027A			
; CURRENT APPLICATION NUMBER: US/10/309,762			
; CURRENT FILING DATE: 2002-12-02			
; PRIOR APPLICATION NUMBER: 60/337275			
; PRIOR FILING DATE: 2001-12-03			
; NUMBER OF SEQ ID NOS: 246			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 110			
; LENGTH: 429			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-309-762-110			
Query Match 78.3%; Score 267.8; DB 16; Length 429;			
Best Local Similarity 87.4%; Pred. No. 4.7e-78;			
Matches 312; Conservative 0; Mismatches 27; Indels 18; Gaps 1;			
Qy	4	GAGTCTGGCCACGAGCTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGCACCTGTCTCT	63
Db	73	GAGTGGGCCACGAGCTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGCACCTGTCTCT	132
Qy	64	GGTGGCTCCATCCGACGTGGTGTTATTACTGGAGTTGGATCCGCCAGCGTCCAGGAAG	123
Db	133	GGTGGCTCCATCAGCAGTGGTGGTTACTACTGGAGCTGGATCCGCCAGCACCCAGGGAAG	192
Qy	124	GGCCTCGAGTGGATCGGTACATCTATCAGTGGGCAACACTTACAAACACCCGTCCTC	183
Db	193	GGCCTCGAGTGGATGGGTACATCTATTACGTGGGAGCACCTTACTACAAACCCGTCCTC	252
Qy	184	AAGAGTCGAGTTTACCATGTTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGCGTGAGC	243
Db	253	AAGAGTCGAGTTTACCATATCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGCGTGAGC	312
Qy	244	TCGTGACTGTCGCCGACACGGCCGGTGATTACTGTGCGAG-----G	285
Db	313	TCGTGACTGTCGCCGACACGGCCGGTGATTACTGTGCGAGAGAGAAATTACGATATTTTG	372
Qy	286	TCAGATGGGTACACTTTGGACAACTGGGCCACGGGAACCCCTGGTCACCGTCTCTCA	342
Db	373	ACTGGTTTCAACTGGTTTCGACCCCTGGGGCCAGGGAACCCCTGGTCACCGTCTCTCA	429

Search completed: August 13, 2004, 19:18:22
Job time : 761.173 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 00:21:37 ; Search time 48.3636 Seconds
(without alignments)
3924.296 Million cell updates/sec

Title: US-10-027-725A-3

Perfect score: 342

Sequence: 1 ctcgagctcggccaggact.....ccctggtcaccgtctctca 342

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/2/ina/5A COMB.seq:*
- 2: /cgn2_6/ptodata/2/ina/5B COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	267.2	78.1	516	4	US-08-472-087-33
2	263.6	77.1	357	1	US-08-360-125-3
3	263.6	77.1	357	2	US-08-450-578-3
4	263.6	77.1	357	2	US-08-017-628-3
5	263.6	77.1	357	2	US-09-014-880-3
6	263.6	77.1	357	4	US-08-450-363-3
7	257	75.1	631	3	US-08-545-809A-31
8	255.8	74.8	450	4	US-09-582-337-13
9	251.8	73.6	1567	3	US-09-049-672A-17
10	245.8	71.9	1543	4	US-09-800-729-74
11	241.8	70.7	366	1	US-08-360-125-9
12	241.8	70.7	366	2	US-08-450-578-9
13	241.8	70.7	366	2	US-09-017-628-9
14	241.8	70.7	366	2	US-09-014-880-9
15	241.8	70.7	366	4	US-08-450-363-9
16	237.8	69.5	1212	3	US-08-545-809A-61
17	233	68.1	800	3	US-08-545-809A-39
18	226.2	66.1	840	3	US-09-260-527-4
19	224.8	65.7	403	3	US-09-042-353-357
20	224.8	65.7	403	4	US-08-758-417A-205
21	220.8	64.6	288	3	US-08-851-362D-7
22	218.6	63.9	732	4	US-10-039-785-56
23	217.8	63.7	357	2	US-08-652-816A-20
24	216.8	63.4	524	3	US-09-042-353-419
25	216.8	63.4	524	4	US-08-758-417A-219
26	216.8	63.4	4926	3	US-09-042-353-418
27	216.8	63.4	4926	4	US-08-758-417A-268

28 216.2 63.2 291 3 US-08-851-362D-11 Sequence 11, Appl
29 215.8 63.1 750 3 US-08-545-809A-59 Sequence 59, Appl
30 215.6 63.0 750 4 US-10-039-785-62 Sequence 62, Appl
31 215.4 63.0 624 3 US-08-545-809A-28 Sequence 28, Appl
32 214.2 62.6 404 4 US-09-042-353-355 Sequence 355, App
33 214.2 62.6 404 4 US-08-758-417A-203 Sequence 203, App
34 212.8 62.2 294 3 US-08-851-362D-3 Sequence 3, Appl
35 212.6 62.2 650 3 US-08-545-809A-4 Sequence 4, Appl
36 211.4 61.8 402 1 US-08-259-372A-5 Sequence 5, Appl
37 211.4 61.8 402 1 US-08-468-671-5 Sequence 5, Appl
38 211 61.7 800 3 US-08-545-809A-55 Sequence 55, Appl
39 210.6 61.6 354 2 US-08-652-816A-23 Sequence 23, Appl
40 209.2 61.2 381 2 US-08-477-553A-45 Sequence 45, Appl
41 208.8 61.1 291 3 US-08-851-362D-9 Sequence 9, Appl
42 208.6 61.0 369 4 US-08-793-450-3 Sequence 3, Appl
43 208.6 61.0 1418 4 US-08-793-450-7 Sequence 7, Appl
44 208.2 60.9 291 3 US-08-851-362D-5 Sequence 5, Appl
45 207.8 60.8 372 2 US-08-477-553A-46 Sequence 46, Appl

ALIGNMENTS

RESULT 1
US-09-472-087-33
; Sequence 33, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GLIMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-472-087-33

Query Match 78.1%; Score 267.2; DB 4; Length 516;
Best Local Similarity 88.6%; Pred. No. 5.8e-76;
Matches 303; Conservative 0; Mismatches 33; Indels 6; Gaps 1;
Qy 7 TCTGCCCCAGACTGGTGAAGCCCTTCACAGACCCCTGTCCTCTCCTGCTCTCTGGT 66
Db 1 TCGGCCCCAGGACTGGTGAAGCCCTTCACAGATCTGTCCTCTCCTGCTCTCTGGT 60
Qy 67 GGCTCCATCCGAGTGGTGGTTATTAATCTGGAGTTGGATCCGCCAGCGTCCAGGAAGGC 126
Db 61 GGCTCCATCAGCAGTGGTGGTCTACTACTGGAGTGGATCCGCCAGCACCAGGAAGGC 120
Qy 127 CTGGAGTGGATCCGGTACATCTATCAGTGGGGAACACCTTACACACCCGTCCTCAAG 186
Db 121 CTGGAGTGGATGGGTGATCTATTAATTTGGGGAACACCTTACTACACCCGTCCTCAAG 180
Qy 187 AGTCAGTTACCATGTCTAGTAGACACCTCTAAGAACACCTTCTCCCTGAGGCTGAGTCT 246
Db 181 AGTCAGTTACCATGTCTAGTAGACACCTCTAAGAACACCTTCTCCCTGAGGCTGAGTCT 240
Qy 247 GTGACTCCGCGGACACGGCGGTGTATTACTGTGCGAGGTGAGATGGG-----TACACT 300
Db 241 GTGACTCCGCGGACACGGCGGTGTATTATTGTGCGAGATAGTGGGGAAGTACTACGGT 300

QY 301 TTGGACAACCTGGGGCAGGAGAACCTGGTGTCAACGGTCTCTCA 342
DB 301 ATAGAGCTCTGGGGCCAGGAGCACCGGTCAACGGTCTCTCA 342

RESULT 2

US-08-360-125-3
; Sequence 3, Application US/08360125
; Patent No. 5767246

GENERAL INFORMATION:

APPLICANT: Saiko HOSOKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5767246ihiko ITO
APPLICANT: Kazuhiro NAGAIKE

TITLE OF INVENTION: Human Monoclonal Antibody

TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer

TITLE OF INVENTION: Cell Membrane

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSER: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500 kb

COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,125

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/905,534

FILING DATE: June 29, 1992

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.

REGISTRATION NUMBER: 33,367

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-8850

TELEFAX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 357 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL:

ANTI-SENSE:

FRAGMENT TYPE:

ORIGINAL SOURCE:

ORGANISM:

STRAIN:

INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:

HAPLOTYPE:

TISSUE TYPE:

CELL TYPE: Hybridoma producing human

CELL TYPE: antibody GAH

CELL LINE:

ORGANELLE:

IMMEDIATE SOURCE:

LIBRARY:

CLONE:

POSITION IN GENOME:

CHROMOSOME/SEGMENT:

MAP POSITION:

UNITS:

FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION:

PUBLICATION INFORMATION:

AUTHORS:

TITLE:

JOURNAL:

VOLUME:

PAGES:

DATE:

DOCUMENT NUMBER:

FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-08-360-125-3

Query Match 77.1%; Score 263.6; DB 1; Length 357;

Best Local Similarity 87.7%; Pred. No. 7e-75;

Matches 300; Conservative 0; Mismatches 39; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACTGCTCT 63
DB 16 GAGTGGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACTGCTCT 75
QY 64 GGTGGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 123
DB 76 GGTGGCTCCATCCAGCAGTTGTGGTTTCTACTGGAACTGGATCCGCCAGCAGCCAGGGAAG 135
QY 124 GGCCTGGAGTGGATCGGOTACATCTATCACAGTGCAACACTACAAACCCGTCCTC 183
DB 136 GGCCTGGAGTGGATTTGGGTACATCTATTACAGTGGGAGCAGCTACTACAAACCCGTCCTC 195
QY 184 AAGAGTCGAGTTACCATGTCTAGTACACACGCTTAAGAACCTCTCTCCCTGAGCGTGAGC 243
DB 196 AAGAGTCGAGTTACCATGTCTAGTACACACGCTTAAGAACCTCTCTCCCTGAGCGTGAGC 255
QY 244 TCTGTGACTGCGGGGACACGGCCGTGTATTACTGTGCGAGGTGAGATGGGTACACTTTG 303
DB 256 TCTGTGACTGCGGGGACACGGCCGTGTATTACTGTGCGAGGTCTACCCGACTACGGGGG 315
QY 304 ---GACAACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342
DB 316 GCTGACTACTGGGGCCAGGGAACAATGGTCAACCGTCTCTCTCA 357

RESULT 3

US-08-450-578-3

; Sequence 3, Application US/08450578

; Patent No. 5837845

GENERAL INFORMATION:

APPLICANT: Saiko HOSOKAWA

APPLICANT: Toshiaki TAGAWA

APPLICANT: Yoko HIRAKAWA

APPLICANT: No. 5837845ihiko ITO

APPLICANT: Kazuhiro NAGAIKE

TITLE OF INVENTION: Human Monoclonal Antibody

TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer

TITLE OF INVENTION: Cell Membrane

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSER: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,578
FILING DATE: May 25, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL TYPE: antibody GAH
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:

NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:

Query Match 77.1%; Score 263.6; DB 2; Length 357;
Best Local Similarity 87.7%; Pred. No. 7e-75;
Matches 300; Conservative 0; Mismatches 39; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACTGCTCT 63
Db |||||
QY 16 GAGTCGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACTGCTCT 75
Db |||||
QY 64 GGTGGCTCCATCCGACAGTGGTGTATTACTGGAGTTGGATCCGCCAGCGTCCAGGAAG 123
Db |||||
QY 76 GGTGGCTCCATCCGACAGTGGTGTATTACTGGAGTTGGATCCGCCAGCGTCCAGGAAG 135
Db |||||
QY 124 GGCCTGGAGTGGATCGGATACATCTATCAGAGTGGGCAACCTTACACACCCGTCCTC 183
Db |||||
QY 136 GGCCTGGAGTGGATCGGATACATCTATCAGAGTGGGAGCACTTACACACCCGTCCTC 195
Db |||||
QY 184 AAGAGTCGAGTTACCATGTGAGTACACAGTCTTAAGAACCACCTTCTCCCTGAGGCTGAGC 243
Db |||||
QY 196 AAGAGTCGAGTTACCATGTGAGTACACAGTCTTAAGAACCACCTTCTCCCTGAGGCTGAGC 255
Db |||||
QY 244 TCTGTGACTGCCCGGACACGGCCGTGTATTACTGTGGAGGTGAGTGGGTACACTTTG 303
Db |||||
QY 256 TCTGTGACTGCCCGGACACGGCCGTGTATTACTGTGGAGGTGAGTGGGTACACTTTG 315
Db |||||
QY 304 ---GACAACTGGGGCCAGGAAACCCCTGGTCAACGCTCTCTCA 342
Db |||||
QY 316 GCTGACTACTGGGGCCAGGAAACATGGTCAACGCTCTCTCA 357
Db |||||

RESULT 4

US-09-017-628-3
; Sequence 3, Application US/09017628
; Patent No. 5990287

GENERAL INFORMATION:
; APPLICANT: HOSOKAWA, Saiko

; APPLICANT: TAGAWA, Toshiaki
; APPLICANT: HIRAKAWA, Yoko

; APPLICANT: ITO, No. 5990287ihiko
; APPLICANT: NAGAIKE, Kazuhiro

; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
; TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; FILE REFERENCE: 177/527361KH

; CURRENT APPLICATION NUMBER: US/09/017,628
; CURRENT FILING DATE: 1998-02-02

; EARLIER APPLICATION NUMBER: 08/360,125
; EARLIER FILING DATE: 1994-12-20

; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3
; LENGTH: 357

; TYPE: DNA
; ORGANISM: Unknown

; FEATURE:
; OTHER INFORMATION: Hybridoma producing human antibody GAH

US-09-017-628-3

Query Match 77.1%; Score 263.6; DB 2; Length 357;

Best Local Similarity 87.7%; Pred. No. 7e-75;

Matches 300; Conservative 0; Mismatches 39; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACTGCTCT 63
Db |||||
QY 16 GAGTCGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACTGCTCT 75
Db |||||
QY 64 GGTGGCTCCATCCGACAGTGGTGTATTACTGGAGTTGGATCCGCCAGCGTCCAGGAAG 123
Db |||||
QY 76 GGTGGCTCCATCCGACAGTGGTGTATTACTGGAGTTGGATCCGCCAGCGTCCAGGAAG 135
Db |||||
QY 124 GGCCTGGAGTGGATCGGATACATCTATCAGAGTGGGCAACCTTACACACCCGTCCTC 183
Db |||||
QY 136 GGCCTGGAGTGGATCGGATACATCTATCAGAGTGGGAGCACTTACACACCCGTCCTC 195
Db |||||
QY 184 AAGAGTCGAGTTACCATGTGAGTACACAGTCTTAAGAACCACCTTCTCCCTGAGGCTGAGC 243
Db |||||
QY 196 AAGAGTCGAGTTACCATGTGAGTACACAGTCTTAAGAACCACCTTCTCCCTGAGGCTGAGC 255
Db |||||
QY 244 TCTGTGACTGCCCGGACACGGCCGTGTATTACTGTGGAGGTGAGTGGGTACACTTTG 303
Db |||||

Db 256 TCTCTGACTGCGCGACACGCGCGTGTATTACTGTGCGAGGTCTACCCGACTACGGGG 315
QY 304 ---GACAACTGGGGCCAGGGAACCCCTGGTCACCGTCTCTCA 342
Db 316 GCTGACTACTGGGGCCAGGGAACATGGTCACCGTCTCTTCA 357

RESULT 5

US-09-014-880-3
; Sequence 3, Application US/09014880
; Patent No. 5990297
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA et al.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
; TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., #800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/014,880
; FILING DATE: January 28, 1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/450,578
; FILING DATE: May 25, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992

ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-721-8200
; TELEFAX: 202-721-8250
; TELEX:

INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; CELL TYPE: Hybridoma producing human
; CELL TYPE: antibody GAH

US-09-014-880-3
Query Match 77.1%; Score 263.6; DB 2; Length 357;
Best Local Similarity 87.7%; Pred. NO. 7e-75;
Matches 300; Conservative 0; Mismatches 39; Indels 3; Gaps 1;

QY 4 GAGTGTGCCAGAGCTGGTGAAGCCTTCACAGACCCCTGTCCTCACTGCACTGTCTCT 63
Db 16 GAGTGTGCCAGAGCTGGTGAAGCCTTCACAGACCCCTGTCCTCACTGCACTGTCTCT 75
QY 64 GGTGGCTCCATCCGAGTGGTGGTATTACTGGAGTGGATCCGCGACGCTCCAGGGAAG 123
Db 76 GGTGGCTCCATCCGAGTGGTGGTATTACTGGAGTGGATCCGCGACGCTCCAGGGAAG 135

QY 124 GGCCTGGAGTGGATCGGGTACATCTATCACAGTGGCAACACCTACAAACCCGTCCTC 183
Db 136 GGCCTGGAGTGGATCGGGTACATCTATCACAGTGGGAGCACCTACTACAAACCCGTCCTC 195
QY 184 AAGAGTCGAGTTTACCATATGTCAGTAGACACGCTCTAGAACCACCTTCTCCCTGAGGCTGAGC 243
Db 196 AAGAGTCGAGTTTACCATATGTCAGTAGACACGCTCTAGAACCACCTTCTCCCTGAGGCTGAGC 255
QY 244 TCTGTGACTGCGCGGACACACGCGCGTGTATTACTGTGCGAGGTGAGATGGGTACACTTTG 303
Db 256 TCTGTGACTGCGCGGACACACGCGCGTGTATTACTGTGCGAGGTGAGATGGGTACACTTTG 315
QY 304 ---GACAACTGGGGCCAGGGAACCCCTGGTCACCGTCTCTCTCA 342
Db 316 GCTGACTACTGGGGCCAGGGAACATGGTCACCGTCTCTTCA 357

RESULT 6

US-08-450-363-3
; Sequence 3, Application US/08450363
; Patent No. 6436434
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 6436434;hiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,363
; FILING DATE: May 25, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992

ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:

INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:

ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL TYPE: antibody GAH
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-363-3

Query Match 77.1%; Score 263.6; DB 4; Length 357;
Best Local Similarity 87.7%; Pred. No. 7e-75;
Matches 300; Conservative 0; Mismatches 39; Indels 3; Gaps 1;

QY 4 GAGTCTGCCCGCAGACTGGTGAAGCCTTCACAGACCTGTCCCTCAGCTGCTCTCT 63
DB 16 GAGTCGGCGCCAGAGCTGGTGAAGCCTTCACAGACCTGTCCCTCAGCTGCTCT 75
QY 64 GGTGGCTCCATCCGCGAGTGGTGGTTTACTGAGTTGGATCCGCGAGCGTCCAGGGAAG 123
DB 76 GGTGGCTCCATCCGCGAGTGGTGGTTTACTGAGTTGGATCCGCGAGCGTCCAGGGAAG 135
QY 124 GGCCTGGAGTGGGTGATCATCTATCAGTGGCAACACCTACAGAACCCGCTCCCTC 183
DB 136 GGCCTGGAGTGGGTGATCATCTATCAGTGGCAACACCTACAGAACCCGCTCCCTC 195
QY 184 AAGAGTCGAGTTACCATCTAGTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
DB 196 AAGAGTCGAGTTACCATCTAGTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 255
QY 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGGAGGTACAGTGGGTACATTTG 303
DB 256 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGGAGGTACAGTGGGTACATTTG 315
QY 304 ---GACAACTGGGCGCAGGGAACCCCTGTGTCACCGTCTCTCA 342
DB 316 GCTGACTACTGGGCGCAGGGAACAAATGGTACCGTCTCTCA 357

US-08-450-363-3

US-08-545-809A-31

Query Match 75.1%; Score 257; DB 3; Length 631;
Best Local Similarity 94.7%; Pred. No. 1.2e-72;
Matches 266; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 4 GAGTCTGCCCGCAGACTGGTGAAGCCTTCACAGACCTGTCCCTCAGCTGCTCTCT 63
DB 305 GAGTCGGCGCCAGAGCTGGTGAAGCCTTCACAGACCTGTCCCTCAGCTGCTCTCT 364
QY 64 GGTGGCTCCATCCGCGAGTGGTGGTTTACTGAGTTGGATCCGCGAGCGTCCAGGGAAG 123
DB 365 GGTGGCTCCATCCGCGAGTGGTGGTTTACTGAGTTGGATCCGCGAGCGTCCAGGGAAG 424
QY 124 GGCCTGGAGTGGGTGATCATCTATCAGTGGCAACACCTACAGAACCCGCTCCCTC 183
DB 425 GGCCTGGAGTGGGTGATCATCTATCAGTGGCAACACCTACAGAACCCGCTCCCTC 484
QY 184 AAGAGTCGAGTTACCATCTAGTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
DB 485 AAGAGTCGAGTTACCATCTAGTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 544
QY 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGGAG 284
DB 545 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGGAG 585

US-08-545-809A-31

RESULT 7

US-08-545-809A-31
Sequence 31, Application US/08545809A
Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE

RESULT 8

US-08-582-337-13
Sequence 13, Application US/09582337
Patent No. 6562618
GENERAL INFORMATION:
APPLICANT: Japan Tobacco, Inc.
TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor

;; TITLE OF INVENTION: and Medicinal Uses Thereof
;; FILE REFERENCE: J1-009PCT
;; CURRENT APPLICATION NUMBER: US/09/582,337
;; PRIOR FILING DATE: 2000-06-23
;; PRIOR APPLICATION NUMBER: JP P1997-367699
;; PRIOR FILING DATE: 1997-12-25
;; PRIOR APPLICATION NUMBER: JP P1998-356183
;; PRIOR FILING DATE: 1998-12-15
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 13
;; LENGTH: 450
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (1)..(450)
;; NAME/KEY: sig_peptide
;; LOCATION: (1)..(58)
;; NAME/KEY: V_region
;; LOCATION: (59)..(353)
US-09-582-337-13

Query Match 74.8%; Score 255.8; DB 4; Length 450;
Best Local Similarity 87.1%; Pred. No. 2.4e-72;
Matches 311; Conservative 0; Mismatches 27; Indels 19; Gaps 2;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCAGCTGCACTGTCTCT 63
Db |||||
74 GAGTCGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCAGCTGCACTGTCTCT 132
QY 64 GGTGGCTCCATCCGACAGTGGTGGTATTACTGGAGTTGGATCCGCGAGCGTCCAGGGAAG 123
Db |||||
133 GGTGGCTCCATCAGACAGTGGTGGTATTACTGGAGTTGGATCCGCGAGCGTCCAGGGAAG 192
QY 124 GGCCTGGAGTGATCGGTGTACATCTATCAGAGTGGCAACCTACAAACCCGTCCTC 183
Db |||||
193 GGCCTGGAGTGATCGGTGTACATCTATCAGAGTGGCAACCTACAAACCCGTCCTC 252
QY 184 AAGAGTCGAGTTACATGTCTAGTAGACACGCTTAAGAACCACTTCCCTCGAGGTGAGC 243
Db |||||
253 AAGAGTCGAGTTACATGTCTAGTAGACACGCTTAAGAACCACTTCCCTCGAGGTGAGC 312
QY 244 TCTGTGACTGCGCGGACACGGCGGTGTATTACTGTGGAGGT----- 286
Db |||||
313 TCTGTGACTGCGCGGACACGGCGGTGTATTACTGTGGAGGTATTACTATAGTGGT 372
QY 287 -CAGATGGGTACACTTTGGACAACTGGGCGCAGGGAACCTGGTCACCGTCTCCTCA 342
Db |||||
373 GGTATTACGACTATTGTACTGTGGGCGCAGGGAACCTGGTCACCGTCTCCTCA 429

RESULT 9
US-09-049-672A-17
; Sequence 17, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guesler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA

;; ZIP: 94304
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/049,672A
;; FILING DATE: HEREWITH
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Cerrone, Michael C
;; REGISTRATION NUMBER: 39,132
;; REFERENCE/DOCKET NUMBER: PF-0497 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650-885-0555
;; TELEFAX: 650-845-4166
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 17:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1567 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: PANTUT01
;; CLONE: 1513264
US-09-049-672A-17

Query Match 73.6%; Score 251.8; DB 3; Length 1567;
Best Local Similarity 84.6%; Pred. No. 7.9e-71;
Matches 302; Conservative 0; Mismatches 37; Indels 18; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCAGCTGCACTGTCTCT 63
Db |||||
150 GAGTCGGGCCAGGACTGGTGAAGCCTTCGAGACCCCTGTCCTCAGCTGCGTGTCTCT 209
QY 64 GGTGGCTCCATCCGACAGTGGTGGTATTACTGGAGTTGGATCCGCGAGCGTCCAGGGAAG 123
Db |||||
210 GGTGGCTCCATCAGTGTGGTGGTATTACTGTGGAGTGGATCCGCGAGCGTCCAGGGAAG 269
QY 124 GGCCTGGAGTGATCGGTGTACATCTATCAGAGTGGCAACCTACAAACCCGTCCTC 183
Db |||||
270 GGCCTGGAGTGATCGGTGTACATCTATCAGAGTGGCAACCTACAAACCCGTCCTC 329
QY 184 AAGAGTCGAGTTACATGTCTAGTAGACACGCTTAAGAACCACTTCCCTCGAGGTGAGC 243
Db |||||
330 AAGAGTCGAGTTACATGTCTAGTAGACACGCTTAAGAACCACTTCCCTCGAGGTGAGC 389
QY 244 TCTGTGACTGCGCGGACACGGCGGTGTATTACTGTGGAGGTGAGT----- 292
Db |||||
390 TCTGTGACTGCGCGGACACGGCGGTGTATTACTGTGGAGGTGAGTATTAGG 449
QY 293 -----GGTACACTTTGGACAACTGGGCGCAGGGAACCTGGTCACCGTCTCCTCA 342
Db |||||
450 GGGGGGAACTACGGTATTGGACGCTCTGGGCGCAGGGAACCTGGTCACCGTCTCCTCA 506

RESULT 10
US-09-800-729-74
; Sequence 74, Application US/09800729
; Patent No. 6605592
; FILE REFERENCE: PZ044P1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: PZ044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22

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; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
; LENGTH: 1543
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-800-729-74

Query Match      71.9%; Score 245.8; DB 4; Length 1543;
Best Local Similarity 83.1%; Pred. No. 6.5e-69;
Matches 280; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 4 GAGTCTGCCCCAGGACTGGTGAAGCCCTTCACAGACCCTGTCCCTCACCTGCACTGTCTCT 63
Db 90 GAGTCTGCCCCAGGACTGGTGAAGCCCTTCACAGACCCTGTCCCTCACCTGCACTGTCTCT 149

QY 64 GTGGCTCCATCCCGAGTGGTGGTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 123
Db 150 GTGGCTCCATCCCGAGTGGTGGTCACTACTGGAGCTGGATCCGCCAGCCAGGGAAG 209

QY 124 GGCTCGAGTGGATCGGGTACATCTATCACAGTGGCAACCTTACAAACCCCGTCCCTC 183
Db 210 GGCTCGAGTGGATGGGTACATCTTACATCGGGTCCACTACTACATCCGTCCTC 269

QY 184 AAGAGTCGAGTTACCATGTCTAGTAGACACGCTTAAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db 270 AAGAGTCGAGTTACCATGTCTAGTAGACACGCTTCTAGAACCACTTCTCCCTGAGGCTGAGC 329

QY 244 TCTGTGACTCCGCGGACACGGCCGTGTATTACTGTGGAGTGCAGTGGGTGACACTTTG 303
Db 330 TCTGTGACTCCGCGGACACGGCCGTGTATTACTGTGGAGATCATCGAGCGACGAGA 389

QY 304 GACAACTGGGSCCAGGGAACCTGGTCAACGCTCTCCT 340
Db 390 GACGGGTACCGTGGATACCGAGGGCTTGACTACT 426

RESULT 11
US-08-360-125-9
; Sequence 9, Application US/08360125
; Patent No. 5767246
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Yoshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5767246hiiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,125
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; APPLICATION NUMBER:

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 366 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human antibody 1-3-1
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-9

Query Match      70.7%; Score 241.8; DB 1; Length 366;
Best Local Similarity 83.2%; Pred. No. 6.7e-68;
Matches 292; Conservative 0; Mismatches 47; Indels 12; Gaps 1;

QY 4 GAGTCTGCCCCAGGACTGGTGAAGCCCTTCACAGACCCTGTCCCTCACCTGCACTGTCTCT 63
Db 16 GAGTCTGCCCCAGGACTGGTGAAGCCCTTCGAGACCCTGTCCCTCACCTGCACTGTCTCT 75

QY 64 GGTGGCTCCATCCCGAGTGGTGGTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 123
Db 76 GGTGGCTCCATCCCGAGTGGTGGTATTACTACTGGGGCTGGATCCGCCAGCCCGCAGGGAAG 135

QY 124 GGCCTGGAGTGGATCGGGTACATCTATCACAGTGGCAACCTTACAAACCCCGTCCCTC 183
Db 136 GGCCTGGAGTGGATCGGGTATCTATTATAGTGGGAGCACTACTACAAACCCCGTCCCTC 195

QY 184 AAGAGTCGAGTTACCATGTCTAGTAGACACGCTTAAAGAACCACTTCTCCCTGAGGCTGAGC 243
```

Db 196 AAGAGTCGAGTCACCATATCCGTAGACACGTCCAGAAACAGTTCTCCCTGAGCTGAGC 255
QY 244 TCTGTGACCTGCCCGGACACGGCGCTGTATTACTGTGCGA-----GGTCAGAT 291
Db 256 TCTGTGACCGCGACACACGGCTGTGTATTACTGTGCGAGGGGAGCTACGGGGGCTAC 315
QY 292 GGTACACTTTGGACAACCTGGGCGCAGGGAACCCCTGGTCACCGTCTCCCTCA 342
Db 316 TACTACGGTATGGACGCTCTGGGCGCAAGGACACCGTCACCGTCTCCCTCA 366

RESULT 12

US-08-450-578-9
; Sequence 9, Application US/08450578
; Patent No. 5837845
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5837845hiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,578
FILING DATE: May 25, 1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA

HYPOTHETICAL:

ANTI-SENSE:

FRAGMENT TYPE:

ORIGINAL SOURCE:

ORGANISM:

STRAIN:

INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:

HAPLOTYPE:

TISSUE TYPE:

CELL TYPE: Hybridoma producing human antibody 1-3-1

CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-578-9

Query Match 70.7%; Score 241.8; DB 2; Length 366;
Best Local Similarity 83.2%; Pred. No. 6.7e-68;
Matches 292; Conservative 0; Mismatches 47; Indels 12; Gaps 1;

QY 4 GAGTCTGCCCGGAGCTGTGAAGCTTTCACAGACCCCTGTCCCTCACCTGCACTGTCTCT 63
Db 16 GAGTCGGGCGCCAGGACTGTGAAGCTTTCGGAGACCCCTGTCCCTCACCTGCACTGTCTCT 75
QY 64 GGTGCTCCATCCGCGAGTGGTGTATTACTGGAGTTGGATCGCGCAGCGTCCAGGGAAG 123
Db 76 GGTGCTCCATCCAGCAGTAGTAGTTACTTCTGGGCTGGATCCGCGCAGCCCGGAGGAG 135
QY 124 GCGCTGGAGTGGATCGGOTACATCTATCAGAGTGCAACACTACAAACCCGCTCCTC 183
Db 136 GGGCTGGAGTGGATTGGGAGTATCTATTATAGTGGGAGCCTACTACAAACCCGCTCCTC 195
QY 184 AAGAGTCGAGTTACCATCTCAGTACACACGCTTAAGACCACTTCTCCCTGAGGCTGAGC 243
Db 196 AAGAGTCGAGTCACCATATCCGTAGACACGTCCTCAAGAACCCAGTTCTCCCTGAGGCTGAGC 255
QY 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGA-----GGTCAGAT 291
Db 256 TCTGTGACCGCGCGCAGACACGCTGTGTATTACTGTGCGAGGGGAGCTACGGGGGCTAC 315
QY 292 GGTACACTTTGGACAACCTGGGCGCAGGGAACCCCTGGTCACCGTCTCCCTCA 342
Db 316 TACTACGGTATGGACGCTCTGGGCGCAAGGACACCGGTCAACCGTCTCCCTCA 366

RESULT 13

US-09-017-628-9
; Sequence 9, Application US/09017628
; Patent No. 5990287
; GENERAL INFORMATION:
; APPLICANT: HOSOKAWA, Saiko
; APPLICANT: TAGAWA, Toshiaki
; APPLICANT: HIRAKAWA, Yoko
; APPLICANT: ITO, No. 5990287hiko
; APPLICANT: NAGAIKE, Kazuhiro
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
; TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; FILE REFERENCE: 177/527361KH
; CURRENT APPLICATION NUMBER: US/09/017,628
; CURRENT FILING DATE: 1998-02-02
; EARLIER APPLICATION NUMBER: 08/360,125

; EARLIER FILING DATE: 1994-12-20
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: Patent Ver. 2.0
 ; SEQ ID NO 9
 ; LENGTH: 366
 ; TYPE: DNA
 ; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: Hybridoma producing human antibody 1-3-1
 US-09-017-628-9

 Query Match 70.7%; Score 241.8; DB 2; Length 366;
 Best Local Similarity 83.2%; Pred. No. 6.7e-68;
 Matches 292; Conservative 0; Mismatches 47; Indels 12; Gaps 1;

 QY 4 GAGTCGCGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACTGTCTCT 63
 DB 16 GAGTCGCGCCAGGACTGGTGAAGCCTTCGAGACCCCTGTCCTCACCTGCACTGTCTCT 75

 QY 64 GGTGGCTCCATCCGAGTGGTGTATTACTAGAGTTGATCCGCGAGTCCAGGGAG 123
 DB 76 GGTGGCTCCATCCGAGTGGTGTATTACTAGAGTTGATCCGCGAGTCCAGGGAG 135

 QY 124 GGCTGGAGTGGATCGGTATCATCTATCAGTGGCAGACCTACAGAACCCCGTCCCTC 183
 DB 136 GGGCTGGAGTGGATCGGTATCATCTATCAGTGGCAGACCTACAGAACCCCGTCCCTC 195

 QY 184 AAGAGTCGAGTACCATGTCAGTAGACAGTCTTAAGAACCTTCTCCCTGAGGTGAGC 243
 DB 196 AAGAGTCGAGTACCATGTCAGTAGACAGTCTTAAGAACCTTCTCCCTGAGGTGAGC 255

 QY 244 TCTGTGACTCCGCGGACACGGCCGTTATTACTGTGCGA-----GGTCAGAT 291
 DB 256 TCTGTGACTCCGCGGACACGGCCGTTATTACTGTGCGA-----GGTCAGAT 315

 QY 292 GGTACACTTTGACAACTGGGCGCAGGACCCCTGGTACCGTCTCCCTCA 342
 DB 316 TACTACGATGAGCAGTCTGGGCGCAAGGACACCGGTACCGTCTCCCTCA 366

 RESULT 14
 US-09-014-880-9
 ; Sequence 9, Application US/09014880
 ; Patent No. 5990297
 ; GENERAL INFORMATION:
 ; APPLICANT: Saiko HOSOKAWA et al.
 ; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
 ; BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
 ; NUMBER OF SEQUENCES: 42
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
 ; STREET: 2033 K Street, N.W., #800
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20006
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: Wordperfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/014,880
 ; FILING DATE: January 28, 1998
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/450,578
 ; FILING DATE: May 25, 1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/360,125
 ; FILING DATE: December 20, 1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/905,534

OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,363
FILING DATE: May 25, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 366 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL:

ANTI-SENSE:

FRAGMENT TYPE:

ORIGINAL SOURCE:

ORGANISM:

STRAIN:

INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:

HAPLOTYPE:

TISSUE TYPE:

CELL TYPE: Hybridoma producing human antibody 1-3-1

CELL LINE:

ORGANELLE:

IMMEDIATE SOURCE:

LIBRARY:

CLONE:

POSITION IN GENOME:

CHROMOSOME/SEGMENT:

MAP POSITION:

UNITS:

FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION:

PUBLICATION INFORMATION:

AUTHORS:

TITLE:

JOURNAL:

VOLUME:

ISSUE:

PAGES:

DATE:

DOCUMENT NUMBER:

FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-08-450-363-9

Query Match 70.7%; Score 241.8; DB 4; Length 366;

Best Local Similarity 83.2%; Pred. No. 6.7e-68;

Matches 292; Conservative 0; Mismatches 47; Indels 12; Gaps 1;

Qy 4 GAGTCTGCCCGCAGGACTGGTGAAGCCCTTCACAGACCCCTGTCCTCAGCTGACTGTCTCT 63

Db 16 GAGTCCGGCGCCAGGACTGGTGAAGCCCTTCGGAGACCCCTGTCCTCAGCTGACTGTCTCT 75

Qy 64 GGTGGCTCCATCCGAGTGGTGTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 123
Db 76 GGTGGCTCCATCCGAGTGGTGTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 135
Qy 124 GGCCTGGAGTGGATCCGGTACATCTATCACAGTGGCAACACCTTACACACCCGTCCTC 183
Db 136 GGCCTGGAGTGGATCCGGTACATCTATCACAGTGGCAACACCTTACACACCCGTCCTC 195
Qy 184 AAGAGTCGAGTTACCATGTCACTAGTACAGTCTAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db 196 AAGAGTCGAGTTACCATGTCACTAGTACAGTCTAAGAACCACTTCTCCCTGAGGCTGAGC 255
Qy 244 TCTGTGACTGCCCGGACACGCGGTGTATTACTGTGCGA-----GGTCAGAT 291
Db 256 TCTGTGACTGCCCGGACACGCGGTGTATTACTGTGCGAAGGAGGAGTACGCGGGGTAC 315
Qy 292 GGTACACTTTGGACAACTGGGCGCAGGGAACCCCTGTCACCGTCTCTCTCA 342
Db 316 TACTACGGTATGGACGCTCTGGGCGCAAGGAGCACCGTCACTCTCTCA 366

Search completed: August 13, 2004, 07:18:08

Job time : 49.3636 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 12, 2004, 19:27:23 ; Search time 1368.2 Seconds
(without alignments)
10073.859 Million cell updates/sec

Title: US-10-027-725A-4
Perfect score: 318
Sequence: 1 gagctcaactcagttccatc.....ccaaagtgagatcaaacga 318

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_on.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_or.*
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- 23: em_pat.*
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- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
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- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	318	100.0	318	9	HSA458379	AJ458379 Homo sapi
2	290.8	91.4	322	9	HUMIGHGD	L03142 Homo sapien
3	290.8	91.4	326	9	HUMIGHGY	L03160 Homo sapien
4	289.2	90.9	796	9	AB064138	AB064138 Homo sapi
5	287.6	90.4	321	6	AR161027	AR161027 Sequence
6	286.6	90.1	324	9	AB063929	AB063929 Homo sapi
7	286.6	90.1	828	9	AB064098	AB064098 Homo sapi
8	286	89.9	321	9	HSIGVK16F	X73855 H.sapiens m
9	286	89.9	328	9	HUMIGHHC	L03184 Homo sapien
10	284.4	89.4	324	9	AB095286	AB095286 Homo sapi
11	284	89.3	369	12	AF453186	AF453186 Synthetic
12	282.8	88.9	324	9	AB063932	AB063932 Homo sapi
13	282	88.7	321	9	AY240163	AY240163 Homo sapi
14	281.8	88.6	324	9	AB095281	AB095281 Homo sapi
15	281.2	88.4	321	6	AR160973	AR160973 Sequence
16	281.2	88.4	321	6	AR160980	AR160980 Sequence
17	281.2	88.4	321	6	AR161046	AR161046 Sequence
18	281.2	88.4	321	9	HSIGVK110	X73860 H.sapiens m
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20	280.4	88.2	321	6	E12913	E12913 Human cDNA
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22	280.2	88.1	387	12	AF453148	AF453148 Synthetic
23	279.6	87.9	321	6	AR160978	AR160978 Sequence
24	279.6	87.9	321	6	AR160984	AR160984 Sequence
25	279.6	87.9	321	6	AR161049	AR161049 Sequence
26	279.6	87.9	321	6	AR161050	AR161050 Sequence
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34	278	87.4	809	9	AB064079	AB064079 Homo sapi
35	277.6	87.3	324	6	BD181714	BD181714 Human-ty
36	277.6	87.3	324	6	BD181715	BD181715 Human-ty
37	277.6	87.3	333	6	BD097236	BD097236 A therape
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40	277.2	87.2	314	9	AY062338	AY062338 Homo sapi
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44	277	87.1	324	9	AF035037	AF035037 Homo sapi
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ALIGNMENTS

RESULT 1
HSA458379 HSA458379 318 bp mRNA linear PRI 30-APR-2002
LOCUS Homo sapiens partial mRNA for immunoglobulin kappa light chain
DEFINITION variable region (IGKV gene), clone 94.
ACCESSION AJ458379
VERSION AJ458379.1 GI:20387057
KEYWORDS IGKV gene; immunoglobulin kappa; light chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
AUTHORS Flicker,S., Steinberger,P., Norderhaug,L., Sperr,W.R., Majlesi,Y.,
Valent,P., Kraft,D. and Valenta,R.

TITLE Conversion of grass allergen-specific human IgE into a protective
IgG1 antibody
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 318)
AUTHORS Flicker, S.
TITLE Direct Submission
JOURNAL Submitted (24-APR-2002) Flicker S., Department of Pathophysiology,
General Hospital of Vienna, 3Q, Waehringer Guertel 18-20, A-1090
Vienna, AUSTRIA

FEATURES

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QY 301 AAGGTGGAGATCAAAACGA 318
Db 301 AAGGTGGAGATCAAAACGA 318

RESULT 2

HUMIGHGD
LOCUS Homo sapiens cell-type T-cell immunoglobulin gamma-chain, V region
DEFINITION (IGHV) mRNA, partial cds.
ACCESSION L03142
VERSION L03142.1 GI:185377
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE

AUTHORS Collet, T.A., Roben, P., O'Kennedy, R., Barbas, C.F. III, Burton, D.R.
and Lerner, R.A.
TITLE A binary plasmid system for shuffling combinatorial antibody
libraries
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10026-10030 (1992)
MEDLINE 93066172
PUBMED 1438192

FEATURES

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QY 181 AGTGGCAGTGGATATGGACAGACTTCACTCTCACCATCAGCAGTCTCAGCCTGAAGAT 240
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QY 241 TTTGCAAGTTACTACTGTCAAGAGAGTCTAGTGGCTCGTACACTTTTGGCCAGGGACC 300
Db 241 TTTGCAAGTTACTACTGTCAAGAGAGTCTAGTGGCTCGTACACTTTTGGCCAGGGACC 300
QY 301 AAGGTGGAGATCAAAACGA 318
Db 301 AAGGTGGAGATCAAAACGA 318

RESULT 3

HUMIGHGY
LOCUS Homo sapiens cell-type T-cell immunoglobulin gamma-chain, V region
DEFINITION (IGHV) mRNA, partial cds.
ACCESSION L03160
VERSION L03160.1 GI:185395


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KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
              Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 326)
AUTHORS      Collet, T.A., Roben, P., O'Kennedy, R., Barbas, C.F. III, Burton, D.R.
              and Lerner, R.A.
TITLE        A binary plasmid system for shuffling combinatorial antibody
              libraries
JOURNAL       Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10026-10030 (1992)
MEDLINE       93066172
PUBMED       1438192
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  Matches 301; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
Qy  1 GAGCTCACTCAGTCCATCTCCCTGTCGATCTGTGGGAGACAGAGTCCACATCAGT 60
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Qy  301 AAGGTGGAGATCAAAACGA 318
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LOCUS      AB064138
DEFINITION Homo sapiens IGH mRNA for immunoglobulin kappa light chain VLJ

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region, partial cds, clone:K97.
AB064138
VERSION     GI:21669482
KEYWORDS
SOURCE
ORGANISM    Homo sapiens (human)
REFERENCE   1 (bases 1 to 796)
AUTHORS      Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M.,
              Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J.,
              Miura, K. and Kurosawa, Y.
TITLE        Construction and characterization of antibody libraries: isolation
              of therapeutic human antibodies and application to functional
              genomics
JOURNAL       Unpublished
REFERENCE     2 (bases 1 to 796)
AUTHORS      Kurosawa, Y.
TITLE        Direct Submission
JOURNAL       Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
              Comprehensive Medical Science, Fujita Health University;
              Kutsukake-cho, Toyooka 470-1192, Japan
              (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
              Please visit our web site
              URL:http://www.fujita-hu.ac.jp/immunity/.
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RESULT 5
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LOCUS   AR161027          321 bp      DNA          linear      PAT 17-OCT-2001
DEFINITION Sequence 199 from patent US 6255455.
ACCESSION AR161027
VERSION   AR161027.1  GI:16226382
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unknown.
REFERENCE 1. (bases 1 to 321)
AUTHORS   Siegel,D.L.
TITLE     Rh(D)-binding proteins and magnetically activated cell sorting
          method for production thereof
JOURNAL   Patent: US 6255455-A 199 03-JUL-2001;
FEATURES  Location/Qualifiers
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QY      301 AAGGTGGAGATCAAAACGA 318
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RESULT 6
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DEFINITION Homo sapiens IGK mRNA for immunoglobulin kappa light chain VLJ
ACCESSION AB063929
VERSION   AB063929.1  GI:21669064
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1
AUTHORS   Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
          Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,

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TITLE
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 324)
AUTHORS Kurosawa,Y.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University;
Kutsukake-cho, Toyosake 470-1192, Japan
(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/.
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Best Local Similarity 94.0%; Pred. No. 4.2e-83;
Matches 298; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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RESULT 7
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LOCUS   AB064098          828 bp      mRNA          linear      PRI 02-JUL-2002
DEFINITION Homo sapiens IGK mRNA for immunoglobulin kappa light chain VLJ
ACCESSION AB064098
VERSION   AB064098.1  GI:21669402
KEYWORDS

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SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M.,
 Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J.,
 Miura, K. and Kurosawa, Y.
 TITLE Construction and characterization of antibody libraries: isolation
 of therapeutic human antibodies and application to functional
 genomics
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 828)
 AUTHORS Kurosawa, Y.
 TITLE Direct Submission
 JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
 Comprehensive Medical Science, Fujita Health University;
 Kutsukake-cho, Toyosake 470-1192, Japan
 (E-mail: kurosawa@fujita-hu.ac.jp, Tel: 81-562-93-9387)
 COMMENT Please visit our web site
 URL: http://www.fujita-hu.ac.jp/immunity/
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 Best Local Similarity 94.0%; Pred. No. 4.2e-83;
 Matches 298; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 2 AGCTCACTCAGTCTCCATCCCTCCTGCTGTGCATCTGTGGGACAGAGTCACCATCAGTT 61
 Db 74 AGATGACCACTCTCCATCCCTCCTGCTGTGCATCTGTAGGACAGAGTCACCATCATT 133

Qy 62 GCCGGCAAGTCACAGAAATTACACCTATTAAATTGGTATCAGCATAAACCGGGAAG 121
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Qy 122 CCCCTAAGCTCCTGATCTATCTGATCTGATCCAGTTTGCAGAGGGGTCCCATCAGGTTCA 181
 Db 194 CCCCTAAGCTCCTGATCTATCTGATCTGATCCAGTTTGCAGAGGGGTCCCATCAGGTTCA 253

Qy 182 GTGCAGTGGATATGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCTCAAGATT 241
 Db 254 GTGCAGTGGATCTGGACAGATTTCATCTCACCATCAGCAGTCTGCACCTCAAGATT 313

Qy 242 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCTCGTACACTTTTGGCCAGGGACCA 301
 Db 314 TTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGGTACACTTTTGGCCAGGGACCA 373

Qy 302 AGTGGAGATCAACGA 318
 Db 374 AGCTGGAGATCAACGA 390

RESULT 8
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 LOCUS H.sapiens mRNA for Ig kappa light chain variable region
 DEFINITION (V-J), subgroup 1.
 ACCESSION X73855
 VERSION X73855.1 GI:516316
 KEYWORDS autoantibody; Ig J-segment; Ig kappa light chain; Ig subgroup I; Ig
 variable region; immunoglobulin.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 321)
 AUTHORS Hexham, J.M., Furmaniak, J., Pegg, C., Burton, D.R. and Smith, B.R.
 TITLE Cloning of a human autoimmune response: preparation and sequencing
 of a human anti-thyroglobulin autoantibody using a combinatorial
 approach
 JOURNAL Autoimmunity 12 (2), 135-141 (1992)
 MEDLINE 92314301
 PUBMED 1617110
 REFERENCE 2 (bases 1 to 321)
 AUTHORS Hexham, J.M., Partridge, L.J., Furmaniak, J., Petersen, V.B.,
 Colls, J.C., Pegg, C., Rees Smith, B. and Burton, D.R.
 TITLE Cloning and characterisation of TPO autoantibodies using
 combinatorial phage display libraries
 JOURNAL Autoimmunity 17 (3), 167-179 (1994)
 MEDLINE 95035699
 PUBMED 7524700
 REFERENCE 3
 AUTHORS Hexham, J.M., Partridge, L.J., Furmaniak, J., Petersen, V.B.,
 Colls, J.C., Pegg, C.A.S., Rees-Smith, B. and Burton, D.R.,
 TITLE Probing the human anti-thyroid peroxidase repertoire of a
 Hashimoto's thyroiditis patient using combinatorial phage display
 libraries
 JOURNAL Eur. J. Immunol.
 REFERENCE 4 (bases 1 to 321)
 AUTHORS Hexham, J.
 TITLE Direct Submission
 JOURNAL Submitted (25-JUN-1993) J. Hexham, Univ. of Sheffield, Dept. of
 Mol. Biology and Biotechnology, P. O. Box 594, Firth Court, Western
 Bank, Sheffield S10 2UH, UK
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V_region
 Query Match 89.9%; Score 286; DB 9; Length 321;
 Best Local Similarity 93.7%; Pred. No. 6.6e-83;
 Matches 298; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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Qy 61 TGCCGGCAAGTCAGAAATTACACCTATTAAATTGGTATCAGCATAAACCGGAAA 120

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Db      121  GCCCTAAGCTCTGATCTATCTGATCCAGTCTTGGAAAGTGGGTCCTCATCAAGGTTTC 180
QY      181  AGTGCAGTGGATATGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCTGAAGAT 240
Db      181  AGTGCAGTGGATCTGGACAGATTTCACCTCTCACCATCAGCAGTCTGCAGCTGAAGAT 240
QY      241  TTTGCAAGTTACTACTGTCAAGAGAGTCTCACTCTCGTCTCGTACACTTTTGGCCAGGGACC 300
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QY      301  AAGGTGGAGATCAAAACGA 318
Db      301  AAGCTGGAGATCAAAACGA 318

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RESULT 9
LOCUS   HUMIGHHC
DEFINITION Homo sapiens cell-type T-cell immunoglobulin gamma-chain, V region (IGHV@) mRNA, partial cds.
ACCESSION L03164
VERSION   L03164.1 GI:185339
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS   Collet,T.A., Roben,P., O'Kennedy,R., Barbas,C.F. III, Burton,D.R. and Lerner,R.A.
TITLE     A binary plasmid system for shuffling combinatorial antibody libraries
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10026-10030 (1992)
MEDLINE   93066172
PUBMED    1438192

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V_region
Query Match      89.9%; Score 286; DB 9; Length 328;
Best Local Similarity 93.7%; Pred. No. 6.6e-83;
Matches 298; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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QY      1  GAGCTCACTCAGTCTCCATCTCCTCGTCTGATCTGTAGGAGACAGAGTCACCATCACT 60

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Db      1  GAGCTCACTCAGTCTCCATCTCCTCGTCTGATCTGTAGGAGACAGAGTCACCATCACT 60
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Db      121  GCCCTAAGCTCTGATCTATCTGCTCATCCAGTTTGGCAAGTGGGTCCTCATCAAGGTTTC 180
QY      181  AGTGCAGTGGATATGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCTGAAGAT 240
Db      181  AGTGCAGTGGATCTGGACAGATTTCACCTCTCACCATCAGCAGTCTGCAGCTGAAGAT 240
QY      241  TTTGCAAGTTACTACTGTCAAGAGAGTCTCACTCTCGTCTCGTACACTTTTGGCCAGGGACC 300
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Db      301  AAGCTGGAGATCAAAACGA 318

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RESULT 10
LOCUS   AB095286
DEFINITION Homo sapiens VL mRNA for immunoglobulin kappa light chain, partial cds. V region, clone:L-LA10.
ACCESSION AB095286
VERSION   AB095286.1 GI:33235623
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS   Tachibana,H., Watanabe,K., Cheng,X.J., Teukamoto,H., Kaneda,Y., Takeuchi,T., Ihara,S. and Petri Jr,W.A. Jr.
TITLE     VH3 Gene Usage in Neutralizing Human Antibodies Specific for the Entamoeba histolytica Gal/GalNAc Lectin Heavy Subunit
JOURNAL   Infect. Immun. 71 (8), 4313-4319 (2003)
PUBMED    12874307
REFERENCE 2 (bases 1 to 324)
AUTHORS   Tachibana,H.
TITLE     Direct Submision
JOURNAL   Submitted (02-NOV-2002) Hiroshi Tachibana, Tokai University School of Medicine, Department of Infectious Diseases, Bohseidai, Isehara, Kanagawa 259-1193, Japan (E-mail:htachiba@is.icc.u-tokai.ac.jp, Tel:81-463-93-1121(ex.2603), Fax:81-463-95-5450)

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FEATURES             Location/Qualifiers
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Query Match      89.4%; Score 284.4; DB 9; Length 324;

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Db	212	GTGGCAGTGGATCTGGGACAGATTTCATCTCACCATCAGCAGCTGTCNACCTGAAGATT	271
Qy	242	TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCACGGGGACCA	301
Db	272	TTGCAACTTACTACTGTCAACAGAGTACAGTACCCCGTACACTTTTGGCCACGGGGACCA	331
Qy	302	AGTGGAGATCAAACG	317
Db	332	AAGTGGATATCAAACG	347

ORGANISM	Homo sapiens Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1
AUTHORS	Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M., Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J., Miura, K. and Kurosawa, Y.
TITLE	Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional genomics
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 324)
AUTHORS	Kurosawa, Y.
TITLE	Direct Submission
JOURNAL	Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University; Katsukake-cho, Toyooka 470-1192, Japan (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387) Please visit our web site URL: http://www.fujita-hu.ac.jp/immunity/ . Location/Qualifiers
COMMENT	
FEATURES	

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ORIGIN
Query Match 88.9%; Score 282.8; DB 9; Length 324;
Best Local Similarity 93.1%; Pred. No. 7.5e-82;
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Best Local Similarity 93.1%; Pred. No. 1.6e-81;
Matches 295; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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QY 62 GCCGGGCAAGTCAGAGATTACACCTATTTAAATTGGTATCAGCATAAACCGGGAAG 121
Db 68 GCCGGGCAAGTCAGAGATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCGGGAAG 127
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Db 128 CCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGTCCCATCAAGGTTCA 187
QY 182 GTGGCAGTGGATATGGGACAGACTTCACCTCACCATCAGCAGTCTGCAGCTGAAGATT 241
Db 188 GTGGCAGTGGATCTGGGACAGATTTCCTCTCACCATCAGCAGTCTGCAACCTGAAGATT 247
QY 242 TTGCAAGTTACTCTGTCAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGGACCA 301
Db 248 TTGCAACTTACTCTGTCAGAGATTAGCTACCTACCCCCACACTTTTGGCCAGGGGACCA 307
QY 302 AGGTGGAGATCAAAACGA 318
Db 308 AGCTGGAGATCAAAACGA 324

RESULT 15
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LOCUS ARI60973 321 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 102 from patent US 6255455.
ACCESSION ARI60973
VERSION ARI60973.1 GI:16226189
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 321)
AUTHORS Siegel, D.L.
TITLE Rn(D)-binding proteins and magnetically activated cell sorting
method for production thereof
JOURNAL Patent: US 6255455-A 102 03-JUL-2001;
FEATURES
Location/Qualifiers
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ORIGIN

Query Match 88.4%; Score 281.2; DB 6; Length 321;
Best Local Similarity 92.8%; Pred. No. 2.5e-81;
Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 GAGCTCACTAGTCTCCATCTCCCTGCTGTCATCTGTGGGAGACAGAGTCACCATCAGT 60
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QY 61 TGCCGGGCAAGTCAGAGATTAAACCTATTTAAATTGGTATCAGCATAAACCGGGAAG 120
Db 64 TGCCGGGCAAGTCAGAGATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCGGGAAG 123
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Db 124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGTCCCATCAAGGTTT 183
QY 181 AGTGGCAGTGATATGGGACAGACTTCACCTCACCATCAGCAGTCTGCAGCTGAAGAT 240
Db 184 AGTGGCAGTGATCTGGGACAGATTTCACCTCACCATCAGCAGTCTGCAACCTGAAGAT 243
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QY 301 AAGGTGGAGATCAAAACGA 318
Db 304 AAGSTGGAAATCAAAACGA 321
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Job time : 1370.2 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 00:12:28 ; Search time 1864.96 Seconds
(without alignments)
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Title: US-10-027-725A-4

Perfect score: 318

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Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_estl:*

9: gb_estl:*

10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_est6:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

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27: em_gss_vxl:*

28: gb_gsst:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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5	277	87.1	487	10	AW405301	UI-HF-BL0
6	275.4	86.6	493	10	AW405753	UI-HF-BL0
7	275.4	86.6	748	14	CB956867	AGENCOURT
8	275.4	86.6	799	14	CB984750	AGENCOURT
9	275.4	86.6	807	14	CB958380	AGENCOURT
10	274.6	86.4	921	12	BG341239	AGENCOURT
11	274	86.2	1067	13	BX397739	AGENCOURT
12	273.8	86.1	498	14	CD684450	EST970 hu
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17	273.8	86.1	797	14	CB987347	AGENCOURT
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19	272.2	85.6	598	14	CD692150	EST8699 h
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28	270.6	85.1	693	14	CD684441	EST1961 hu
29	269	84.6	391	10	AW404992	UI-HF-BL0
30	269	84.6	483	14	CD699627	EST16023
31	269	84.6	708	14	CB956923	AGENCOURT
32	269	84.6	738	14	CB987788	AGENCOURT
33	269	84.6	742	14	CB984723	AGENCOURT
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35	269	84.6	793	14	CB987506	AGENCOURT
36	269	84.6	807	14	CB957785	AGENCOURT
37	269	84.6	855	14	CB995312	AGENCOURT
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ALIGNMENTS

RESULT 1
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DEFINITION
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IMAGE:3057288 5', mRNA sequence.
ACCESSION
AW405752
VERSION
AW405752.1 GI:6924809
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 447)
NIH-MGC <http://mgi.nci.nih.gov/>
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapps-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

Seq primer: M13 Forward.	Location/Qualifiers																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/notes="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

ORIGIN
Query Match      87.6%; Score 278.6; DB 14; Length 525;
Best Local Similarity 92.4%; Pred. No. 1.2e-77;
Matches 293; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY  2 AGCTCACTCAGTCTCCATCCCTGCTGTCATCTGTGGGAGACAGAGTCAACATCAGTT 61
Db  124 AGATGACCCAGTCTCCATCCCTGCTGTCATCTGTAGGAGACAGAGTCAACATCAGTT 183
QY  62 GCCGGGCAAGTCAGAGAAATTAACACCTATTAAATTGGTATCAGCATAAACCCAGGAAAG 121
Db  184 GCCGGGCAAGTCAGAGAAATTAACACCTATTAAATTGGTATCAGCATAAACCCAGGAAAG 243
QY  122 CCCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAGGAGTGGGTCCTCAAGGTTCA 181
Db  244 CCCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAGGAGTGGGTCCTCAAGGTTCA 303
QY  182 GTGGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGAGCTGAAGATT 241
Db  304 GTGGCAGTGGATCTGGGACAGATTTCATCTCGCCATCAGCAGTCTGCAACTGAAGATT 363
QY  242 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGGACCA 301
Db  364 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGGACCA 423
QY  302 AGGTGGAGATCAACGA 318
Db  424 ACCTGGAGATCAACGA 440

RESULT 4
CD690145
LOCUS      CD690145      624 bp      mRNA      linear      EST 25-JUN-2003
DEFINITION EST6668 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION  CD690145
VERSION     CD690145.1  GI:32210615
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS     Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
Zeng,Y.-X.
TITLE       Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL     Unpublished (2003)
COMMENT     Contact: YiXin Zeng
            Cancer Center
            Sun Yat-sen University
            651 DongFeng Road East, GuangZhou 510060, China
            Tel: 86-1380-9770-743
            Fax: 86-20-8775-4506
            Email: yxzeng@gzsums.edu.cn.

FEATURES
            source
            1..624
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /tissue_type="normal nasopharynx"
            /clone_lib="human nasopharynx"
            /notes="ESTs generated from a normal nasopharynx cDNA
            library from southern Chinese"

ORIGIN
Query Match      87.6%; Score 278.6; DB 14; Length 624;

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/notes="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

ORIGIN
Best Local Similarity 92.4%; Pred. No. 1.3e-77;
Matches 293; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY  2 AGCTCACTCAGTCTCCATCCCTGCTGTCATCTGTGGGAGACAGAGTCAACATCAGTT 61
Db  121 AGATGACCCAGTCTCCATCCCTGCTGTCATCTGTAGGAGACAGAGTCAACATCAGTT 180
QY  62 GCCGGGCAAGTCAGAGAAATTAACACCTATTAAATTGGTATCAGCATAAACCCAGGAAAG 121
Db  181 GCCGGGCAAGTCAGAGAAATTAACACCTATTAAATTGGTATCAGCATAAACCCAGGAAAG 240
QY  122 CCCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAGGAGTGGGTCCTCAAGGTTCA 181
Db  241 CCCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAGGAGTGGGTCCTCAAGGTTCA 300
QY  182 GTGGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGAGCTGAAGATT 241
Db  301 GTGGCAGTGGATCTGGGACAGATTTCATCTCACCATCAGCAGTCTGCAACTGAAGATT 360
QY  242 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGGACCA 301
Db  361 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGGACCA 420
QY  302 AGGTGGAGATCAACGA 318
Db  421 AGCTGGAGATCAACGA 437

RESULT 5
AW405301
LOCUS      AW405301      487 bp      mRNA      linear      EST 16-FEB-2000
DEFINITION UT-HP-BL0-ack-b-02-0-UI.r1 NIH MGC_37 Homo sapiens cDNA clone
IMAGE:3059259 5', mRNA sequence.
ACCESSION  AW405301
VERSION     AW405301.1  GI:6924358
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS     NIH-MGC http://mgi.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cga@bbs-kemail.nih.gov
            Eco RI site shown at the beginning of the sequence.
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M.B. Soares Lab
            cDNA Library Arrayed by: M.B. Soares Lab
            DNA sequencing by: M.B. Soares Lab
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.

FEATURES
            Location/Qualifiers
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            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:3059259"
            /tissue_type="lymph"
            /cell_type="germinal center B cells"
            /cell_line="MGC85"
            /lab_host="DH10B (LT1)"
            /clone_lib="NIH MGC 37"
            /note="Vector: pTZ19-Pac; Site 1: NotI; Site 2: Eco RI;
            Constructed from size fractionated cytoplasmic mRNA
            (1.5-2.5kb). Directionally cloned. Cells provided by Louis
            M. Staudt, Ph.D. Library preparation by Maria de Fatima
            Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN
```

Query Match 87.1%; Score 277; DB 10; Length 487;
Best Local Similarity 92.1%; Pred. No. 3.7e-77; Indels 0; Gaps 0;
Matches 292; Conservative 0; Mismatches 25;

QY 2 AGCTCACTCAGTCTCCATCCCTCCCTGCTGTCATCTGTGGGAGACAGAGTCCACATCACTT 61
|||
DB 49 AGATGACCCAGTCGGCATCCTCCCTGCTGTCATCTGTAGGAGACAGAGTCCACATCACTT 108
|||
QY 62 GCCGGGCAAGTCAGAGATTAACACCTATTTAAATTTGGTATCAGCATAAACAGGGAAG 121
|||
DB 109 GCCGGGCAAGTCAGAGCATTAAGCAGCTATTTAAATTTGGTATCAGCAGAAACAGGGAAG 168
|||
QY 122 CCCCTAAGCTCTGATCTGTCATCCAGTTTGCAAAAGTGGGTCCCATCAAGTTTCA 181
|||
DB 169 CCCCTAATCTCTGATTTATGTTGATCCATTTTGCAAAAGTGGGTCCCATCAAGTTTCA 228
|||
QY 182 GTGGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCTCGAAGATT 241
|||
DB 229 GTGGCAGTGGATCTGGGACAGATTCTCTCACCATCAGCAGTCTGCAACTCGAAGATT 288
|||
QY 242 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGGCTCTGTACACTTTTGGCCAGGGGACCA 301
|||
DB 289 TTGCAACTTACTACTGTCAACAGAGTTACAGTGGCCCGTACAGTTTTCGCCAGGGGACCA 348
|||
QY 302 AGGTGGAGATCAAAACGA 318
|||
DB 349 AGCTAGATCAAAACGA 365
|||

RESULT 6
AW405753 493 bp mRNA linear EST 16-FEB-2000
LOCUS UI-HF-BLO-abp-a-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
DEFINITION IMAGE:3057290 5', mRNA sequence.
ACCESSION AW405753
VERSION AW405753.1 GI:6924810
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES
source
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3057290"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH MGC 37"
/note="Vector: pTV73-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 86.6%; Score 275.4; DB 10; Length 493;
Best Local Similarity 91.8%; Pred. No. 1.2e-76; Indels 0; Gaps 0;
Matches 291; Conservative 0; Mismatches 26;

QY 2 AGCTCACTCAGTCTCCATCCCTCCCTGCTGTCATCTGTGGGAGACAGAGTCCACATCACTT 61
|||
DB 79 AGATGACCCAGTCTCCATCCCTCCCTGCTGTCATCTGTAGGAGACAGAGTCCACATCACTT 138
|||
QY 62 GCCGGGCAAGTCAGAGATTAACACCTATTTAAATTTGGTATCAGCATAAACAGGGAAG 121
|||
DB 139 GCCGGGCAAGTCAGAGCATTAAGCAGCTATTTAAATTTGGTATCAGCAGAAACAGGGAAG 198
|||
QY 122 CCCCTAAGCTCTGATCTGTCATCCAGTTTGCAAAAGTGGGTCCCATCAAGTTTCA 181
|||
DB 199 CCCCTAAGCTCTGATCTGTCATCCAGTTTGCAAAAGTGGGTCCCATCAAGTTTCA 258
|||
QY 182 GTGGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCTCGAAGATT 241
|||
DB 259 GTGGCAGTGGATCTGGGACAGATTCTCTCACCATCAGCAGTCTGCAACTCGAAGATT 318
|||
QY 242 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGGCTCTGTACACTTTTGGCCAGGGGACCA 301
|||
DB 319 TTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCGCAGCTTCGCCAAGGGACCA 378
|||
QY 302 AGGTGGAGATCAAAACGA 318
|||
DB 379 AGGTGGAATCAAAACGA 395
|||

RESULT 7
CB956867 748 bp mRNA linear EST 29-APR-2003
LOCUS AGENCOURT_13778741 NIH_MGC_184 Homo sapiens cDNA clone
DEFINITION IMAGE:30351770 5', mRNA sequence.
ACCESSION CB956867
VERSION CB956867.1 GI:30212984
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: NDCM149 row: n column: 03
High quality sequence stop: 528.

FEATURES
source
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30351770"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
SfiI (ggccattggcc); Site_2: SfiI (ggccctcgcc);
Library is oligo-dr primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyroid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGGCCCATTTATGGC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGCGAGCGCCGACATG-dT(30)BN-3' (where B = A,

C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

```

ORIGIN
Query Match      86.6%; Score 275.4; DB 14; Length 748;
Best Local Similarity 91.8%; Pred. No. 1.6e-76;
Matches 291; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 2 AGCTCACTCAGTCCATCCCTCCCTGCTGTCATCTGTGGGAGACAGAGTCAACATCAGTT 61
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 102 AGATGACCACTCTCCATCCCTCCCTGCTGTCATCTGTAGGAGACAGAGTCAACATCATT 161
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 62 GCCGGGCAAGTCAGAGAAATTAACACCTATTAAATTTGGTATCAGCATAAACAGGGAAG 121
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 122 CCCCTAAGCTCCTGATCTATCTGCATCCAGTTTGCAGAGTGGGTCCTCATCAAGTTCA 181
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 222 CCCCTAACCTCCTGATCTATCTGCTGATCCAGTTTGCAGAGTGGGTCCTCATCAAGTTCA 281
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 182 GTGCAGTGGATATGGGACAGACTTCACTCTCAACATCAGCAGTCTGCAGCTCTGAAGATT 241
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 282 GTGCAGTGGATATGGGACAGACTTCACTCTCAACATCAGCAGTCTGCAGCTCTGAAGATT 341
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 242 TTGCAAGTACTACTGTCAAGAGAGTCTGAGTGGCTGTGATCACTTTGGCCAGGGACCA 301
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 342 CTGCAACTTACTACTGTCAACAGAGTCAAGTACCCCTTGGACTTTGGCCAGGGACCA 401
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 302 AGTGGAGATCAACGA 318
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 402 AGCTGGAGATCAACGA 418
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
CB984750 799 bp mRNA linear EST 01-MAY-2003
LOCUS
DEFINITION
AGENCOURT_13574990 NIH MGC 184 Homo sapiens cDNA clone
IMAGE:30326373 5', mRNA sequence.
CB984750
ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 799)
NTH-MGC http://mgi.nci.nih.gov/
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
UNPUBLISHED (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM133 row: k column: 22
High quality sequence stop: 412.
Location/Qualifiers
1. 799
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:30326373"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NIH MGC 184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site:1:
SfiI (ggccattatggcc); Site 2: SfiI (ggccgctcggcc);

FEATURES
source
1. 799
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30326373"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NIH MGC 184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site:1:
SfiI (ggccattatggcc); Site 2: SfiI (ggccgctcggcc);

ORIGIN
Query Match      86.6%; Score 275.4; DB 14; Length 799;
Best Local Similarity 91.8%; Pred. No. 1.6e-76;
Matches 291; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 2 AGCTCACTCAGTCCATCCCTCCCTGCTGTCATCTGTGGGAGACAGAGTCAACATCAGTT 61
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 101 AGATGACCACTCTCCATCCCTCCCTGCTGTCATCTGTAGGAGACAGAGTCAACATCATT 160
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 62 GCCGGGCAAGTCAGAGAAATTAACACCTATTAAATTTGGTATCAGCATAAACAGGGAAG 121
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 161 GCCGGGCAAGTCAGAGAAATTAACACCTATTAAATTTGGTATCAGCATAAACAGGGAAG 220
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 122 CCCCTAAGCTCCTGATCTATCTGCTGATCCAGTTTGCAGAGTGGGTCCTCATCAAGTTCA 181
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 221 CCCCTAAGCTCCTGATCTATCTGCTGATCCAGTTTGCAGAGTGGGTCCTCATCAAGTTCA 280
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 182 GTGCAGTGGATATGGGACAGACTTCACTCTCAACATCAGCAGTCTGCAGCTCTGAAGATT 241
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 281 GTGCAGTGGATATGGGACAGACTTCACTCTCAACATCAGCAGTCTGCAGCTCTGAAGATT 340
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 242 TTGCAAGTACTACTGTCAAGAGAGTCTGAGTGGCTGTGATCACTTTGGCCAGGGACCA 301
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 341 TTGCAAGTACTACTGTCAAGAGAGTCTGAGTGGCTGTGATCACTTTGGCCAGGGACCA 400
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
CB958380 807 bp mRNA linear EST 29-APR-2003
LOCUS
DEFINITION
AGENCOURT_13666601 NIH MGC 184 Homo sapiens cDNA clone
IMAGE:30353194 5', mRNA sequence.
CB958380
ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 807)
NIH-MGC http://mgi.nci.nih.gov/
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
UNPUBLISHED (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM153 row: i column: 11
High quality sequence stop: 532.
Location/Qualifiers
1. 807
/organism="Homo sapiens"
/mol_type="mRNA"

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Library is oligo-dT primed and directionally cloned. cDNA was prepared from a glandular pool of tissues from thyroid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

```

ORIGIN
Query Match      86.6%; Score 275.4; DB 14; Length 799;
Best Local Similarity 91.8%; Pred. No. 1.6e-76;
Matches 291; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 2 AGCTCACTCAGTCCATCCCTCCCTGCTGTCATCTGTGGGAGACAGAGTCAACATCAGTT 61
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 101 AGATGACCACTCTCCATCCCTCCCTGCTGTCATCTGTAGGAGACAGAGTCAACATCATT 160
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 62 GCCGGGCAAGTCAGAGAAATTAACACCTATTAAATTTGGTATCAGCATAAACAGGGAAG 121
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 161 GCCGGGCAAGTCAGAGAAATTAACACCTATTAAATTTGGTATCAGCATAAACAGGGAAG 220
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 122 CCCCTAAGCTCCTGATCTATCTGCTGATCCAGTTTGCAGAGTGGGTCCTCATCAAGTTCA 181
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 221 CCCCTAAGCTCCTGATCTATCTGCTGATCCAGTTTGCAGAGTGGGTCCTCATCAAGTTCA 280
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 182 GTGCAGTGGATATGGGACAGACTTCACTCTCAACATCAGCAGTCTGCAGCTCTGAAGATT 241
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 281 GTGCAGTGGATATGGGACAGACTTCACTCTCAACATCAGCAGTCTGCAGCTCTGAAGATT 340
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 242 TTGCAAGTACTACTGTCAAGAGAGTCTGAGTGGCTGTGATCACTTTGGCCAGGGACCA 301
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 341 TTGCAAGTACTACTGTCAAGAGAGTCTGAGTGGCTGTGATCACTTTGGCCAGGGACCA 400
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
CB958380 807 bp mRNA linear EST 29-APR-2003
LOCUS
DEFINITION
AGENCOURT_13666601 NIH MGC 184 Homo sapiens cDNA clone
IMAGE:30353194 5', mRNA sequence.
CB958380
ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 807)
NIH-MGC http://mgi.nci.nih.gov/
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
UNPUBLISHED (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM153 row: i column: 11
High quality sequence stop: 532.
Location/Qualifiers
1. 807
/organism="Homo sapiens"
/mol_type="mRNA"

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ORIGIN

Query Match 86.1%; Score 273.8; DB 14; Length 499;
 Best Local Similarity 91.5%; Pred. No. 3.9e-76;
 Matches 290; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 2 AGCTCACTCAGTCTCCATCCCTCCCTGCTGTCATCTGTGGGAGACAGAGTCACCATCAGTT 61
 Db 137 AGATGACCCAGTCTCCATCCCTCCCTGCTGTCATCTGTAGGAGACAGAGTCACCATCAGTT 196

QY 62 GCCGGGCAAGTCAGAGATTAACACCTATTTAAATTTGGTATCAGCATAAACAGGGAAG 121
 Db 197 GCCGGGCAAGTCAGAGATTAACACCTATTTAAATTTGGTATCAGCATAAACAGGGAAG 256

QY 122 CCCCTAAGCTCTGATCTATGTCATCCAGTTTCGAAAGTGGGTCCCATCAAGGTTCA 181
 Db 257 CCCCTAAGCTCTGATCTATGTCATCCAGTTTCGAAAGTGGGTCCCATCAAGGTTCA 316

QY 182 GTGGCAGTGGATATGGGACAGACTTCACTCTCAACATCAGCAGTCTGAGCTGAAGATT 241
 Db 317 GTGGCAGTGGATATGGGACAGACTTCACTCTCAACATCAGCAGTCTGAGCTGAAGATT 376

QY 242 TTGCAAGTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGGACCA 301
 Db 377 TTGCAAGTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGGACCA 436

QY 302 AGGTGGAGATCAACGA 318
 Db 437 CGGTGGAGATCAGCA 453

RESULT 14
 AW404714
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

AW404714 608 bp mRNA linear EST 16-FEB-2000
 UL-HF-BLO-acd-c-11-0-UI.r1 NIH MGC_37 Homo sapiens cDNA clone
 IMAGE:3058580 5', mRNA sequence.

AW404714.1 GI:6923771
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: M13 Forward.

FEATURES
 source

1..608
 Location/Qualifiers
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 /mol_type="mRNA"
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 /clone="IMAGE:3058580"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="DH10B (UT1)"
 /clone_lib="NIH MGC 37"
 /note="Vector: pMT3-Pac; Site 1: NotI; Site 2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (1.5-2.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. Library preparation by Maria de Fatima
 Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 86.1%; Score 273.8; DB 10; Length 608;
 Best Local Similarity 91.5%; Pred. No. 4.5e-76;
 Matches 290; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 2 AGCTCACTCAGTCTCCATCCCTCCCTGCTGTCATCTGTGGGAGACAGAGTCACCATCAGTT 61
 Db 49 AGATGACCCAGTCTCCATCCCTCCCTGCTGTCATCTGTAGGAGACAGAGTCACCATCAGTT 108

QY 62 GCCGGGCAAGTCAGAGATTAACACCTATTTAAATTTGGTATCAGCATAAACAGGGAAG 121
 Db 109 GCCGGGCAAGTCAGAGATTAACACCTATTTAAATTTGGTATCAGCATAAACAGGGAAG 168

QY 122 CCCCTAAGCTCTGATCTATGTCATCCAGTTTCGAAAGTGGGTCCCATCAAGGTTCA 181
 Db 169 CCCCTAAGCTCTGATCTATGTCATCCAGTTTCGAAAGTGGGTCCCATCAAGGTTCA 228

QY 182 GTGGCAGTGGATATGGGACAGACTTCACTCTCAACATCAGCAGTCTGAGCTGAAGATT 241
 Db 229 GTGGCAGTGGATATGGGACAGACTTCACTCTCAACATCAGCAGTCTGAGCTGAAGATT 288

QY 242 TTGCAAGTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGGACCA 301
 Db 289 TTGCAAGTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGGACCA 348

QY 302 AGGTGGAGATCAACGA 318
 Db 349 GACTGGAGATCAACGA 365

RESULT 15
 CB959008
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

CB959008 724 bp mRNA linear EST 29-APR-2003
 AGENCOURT 13664954 NIH MGC 184 Homo sapiens cDNA clone
 IMAGE:30354121 5', mRNA sequence.

CB959008
 CB959008.1 GI:30215124
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDCM155 row: p column: 02
 High quality sequence stop: 549.

FEATURES
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 /mol_type="mRNA"
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 /clone="IMAGE:30354121"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 184"
 /note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site 1:
 SfiI (ggccattaggcc); Site 2: SfiI (ggccctctggcc);
 Library is oligo-dT primed and directionally cloned. cDNA
 was prepared from a glandular pool of tissues from thyroid,
 parathyroid, adrenal, cortex and pineal gland. 5' and 3'
 adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CACGCCATTATGGC-3' and 3' adaptor sequence:
 5'-ATCTAGAGCGCGGCGGCACATG-dT(30)BN-3' (where B = A,

C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

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Query Match      86.1%; Score 273.8; DB 14; Length 724;
Best Local Similarity 91.5%; Pred No. 5e-76;
Matches 290; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 2 AGCTCAGTCTCCATCCCTCTGTCATCTGTGGGACAGAGTCACCATCAGTT 61
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 97 AGATGACCCAGTCTCCATCCCTCTGTCATCTGTAGGACAGAGTCATCACTT 156
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 62 GCCGGGCAAGTCAGAGATTACACCTATTTAAATTGGTATCAGCATAAACCAGGAAAG 121
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 157 GCCGGGCAAGTCAGAGATTACACCTATTTAAATTGGTATCAGCATAAACCAGGAAAG 216
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 122 CCCCTAAGCTCCTGATCTATGTCATCCAGTTTGCAAAGTGGGTCCCATCAAGTTCA 181
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 217 CCCCTAAGCTCCTGATCTATGTCATCCAGTTTGCAAAGTGGGTCCCATCAAGTTCA 276
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 182 GTGGCAGTGGATATGGGACAGACTTCACTCTACCATCAGCAGTCTGCAGCTGAAGATT 241
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 277 GTGGCAGTGGATATGGGACAGACTTCACTCTACCATCAGCAGTCTGCAGCTGAAGATT 336
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 242 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACITTTGGCCAGGGGACCA 301
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 337 TTGCAACTTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACITTTGGCCAGGGGACCA 396
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 302 AGGTGGAGATCAAAACGA 318
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 397 AGGTGGAAATCAACGA 413
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Search completed: August 13, 2004, 07:13:23
Job time : 1867.96 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 12, 2004, 11:40:47 ; Search time 207.182 Seconds
(without alignments)
6520.490 Million cell updates/sec

Title: US-10-027-725A-4
Perfect score: 318
Sequence: 1 gagctactcagctccatc.....ccaaagtgagatcaaacga 318

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	318	100.0	318	6	ABK89640 DNA encod
2	287.6	90.4	321	5	Aah68701 Human ant
3	287.6	90.4	321	8	AcD45365 Anti-Rh(D
4	281.2	88.4	321	5	Aah68720 Human ant
5	281.2	88.4	321	5	Aah68654 Human ant
6	281.2	88.4	321	5	Aah68647 Human ant
7	281.2	88.4	321	8	AcD45311 Anti-Rh(D
8	281.2	88.4	321	8	AcD45318 Anti-Rh(D
9	281.2	88.4	321	8	AcD45384 Anti-Rh(D
10	280.4	88.2	321	2	AAT66781 Anti-canc
11	279.6	87.9	321	5	Aah68723 Human ant
12	279.6	87.9	321	5	Aah68658 Human ant
13	279.6	87.9	321	5	Aah68724 Human ant
14	279.6	87.9	321	5	Aah68652 Human ant
15	279.6	87.9	321	8	AcD45388 Anti-Rh(D
16	279.6	87.9	321	8	AcD45387 Anti-Rh(D
17	279.6	87.9	321	8	AcD45316 Anti-Rh(D
18	279.6	87.9	321	8	AcD45322 Anti-Rh(D
19	277.6	87.3	324	7	AAL5120 Human ant
20	277.6	87.3	333	5	Aah74684 Nucleotid
21	277.6	87.3	333	7	ABT34320 Hepatitis
22	277.6	87.3	720	7	ABT34315 Hepatitis
23	277.6	87.3	900	5	Aah74688 Nucleotid

24	277.6	87.3	900	7	ABT34324	Abt34324 Hepatitis
25	277	87.1	396	2	AAT75423	Aat75423 Human ant
26	276.4	86.9	321	5	Aah68713	Aah68713 Human ant
27	276.4	86.9	321	5	AAH68703	Aah68703 Human ant
28	276.4	86.9	321	8	ACD45377	AcD45377 Anti-Rh(D
29	276.4	86.9	321	8	ACD45367	AcD45367 Anti-Rh(D
30	276.2	86.9	324	5	AAH68657	Aah68657 Human ant
31	276.2	86.9	324	5	AAH68712	Aah68712 Human ant
32	276.2	86.9	324	5	AAH68646	Aah68646 Human ant
33	276.2	86.9	324	8	ACD45321	AcD45321 Anti-Rh(D
34	276.2	86.9	324	8	ACD45376	AcD45376 Anti-Rh(D
35	276.2	86.9	324	8	ACD45310	AcD45310 Anti-Rh(D
36	276	86.8	720	2	AAH36070	Aax36070 DNA encod
37	276	86.8	720	7	ABZ76706	Abz76706 Human ser
38	275.4	86.6	341	2	AAT60119	Aat60119 Coding se
39	275.4	86.6	729	3	AAA11630	Aaall630 Human imm
40	275.4	86.6	729	6	ABL46009	AbL46009 Humanised
41	274.8	86.4	321	5	AAH68718	Aah68718 Human ant
42	274.8	86.4	321	5	AAH68650	Aah68650 Human ant
43	274.8	86.4	321	8	ACD45382	AcD45382 Anti-Rh(D
44	274.8	86.4	321	8	ACD45314	AcD45314 Anti-Rh(D
45	274.2	86.2	322	6	ABS62720	ABs62720 Anti-IGF-

ALIGNMENTS

RESULT 1

ID	ABK89640	standard; DNA; 318 BP.
XX	ABK89640	
AC	ABK89640;	
XX		
DT	21-OCT-2002	(first entry)
XX		
DE	DNA encoding human Ige Fab clone 94 light chain.	
XX		
KW	Human; fab; ds; gene; antiallergic; vaccine; grass pollen; Phi p 2;	
KW	timothy grass pollen allergen; passive immunotherapy.	
XX		
OS	Homo sapiens.	
XX		
EH	Key	Location/Qualifiers
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FT	misc_feature	7..63
FT		/*tag= b
FT		/note= "PR1 region"
FT	misc_feature	64..96
FT		/*tag= c
FT		/note= "CDR1 region"
FT	misc_feature	97..141
FT		/*tag= d
FT		/note= "PR2 region"
FT	misc_feature	142..162
FT		/*tag= f
FT		/note= "CDR2 region"
FT	misc_feature	163..258
FT		/*tag= g
FT		/note= "PR3 region"
FT	misc_feature	259..285
FT		/*tag= h
FT		/note= "CDR3 region"
XX		
PD	WO200253595-A1.	
XX		
XX	11-JUL-2002.	
XX		
PF	27-DEC-2001; 2001WO-SE002308.	
XX		
PR	29-DEC-2000; 2000SE-00004892.	
XX		

PA (PHAA) PHARMACIA DIAGNOSTICS AB.
XX
PI Flicker S, Steinberger P, Kraft D, Valenta R;
XX
DR P-PSDB; ABG30448.
XX
DR WPI; 2002-583604/62.
XX
PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
XX variable region of group 2 allergen specific-human IgE Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX
PS Disclosure; Page 34; 45pp; English.
XX
XX This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have anti-allergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The fabs
CC - or a vaccine against a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergic patients
CC IgE antibodies to Phi p 2. The present sequence represents the DNA
CC encoding the human IgG fab, clone 94 light chain protein of the invention
XX
SQ Sequence 318 BP; 84 A; 81 C; 77 G; 76 T; 0 U; 0 Other;

Query Match 100.0%; Score 318; DB 6; Length 318;
Best Local Similarity 100.0%; Pred. No. 7.4e-91;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGCTCAGTCAGTCTCCCTCCCTGCTGTCATCTGTGGGAGACAGAGTCACCATCACT 60
DB 1 GAGCTCAGTCAGTCTCCCTCCCTGCTGTCATCTGTGGGAGACAGAGTCACCATCACT 60
QY 61 TCCCGGCAAGTCAGAGAAATTAACACCTATTAAATTGGTATCAGCATAAACAGGGAAA 120
DB 61 TCCCGGCAAGTCAGAGAAATTAACACCTATTAAATTGGTATCAGCATAAACAGGGAAA 120
QY 121 GCCCTTAAGTCTCTGATCTATGTCATCCAGTTCGAAAGTGGGTGCCATCAAGGTTTC 180
DB 121 GCCCTTAAGTCTCTGATCTATGTCATCCAGTTCGAAAGTGGGTGCCATCAAGGTTTC 180
QY 181 AGTGGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCTGAAGAT 240
DB 181 AGTGGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCTGAAGAT 240
QY 241 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCTGCTGCTACACTTTTGGCCAGGGGACC 300
DB 241 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCTGCTGCTGCTACACTTTTGGCCAGGGGACC 300
QY 301 AAGGTGGAGATCAAAACGA 318
DB 301 AAGGTGGAGATCAAAACGA 318

RESULT 2
AAH68701
ID AAH68701 standard; DNA; 321 BP.
XX
AC AAH68701;
XX
DT 14-SEP-2001 (first entry)
XX
DE Human anti-Rh(D) antibody clone SH13 nucleotide sequence.
XX
KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
red blood cell; Rh phenotype; diagnosis; therapeutic; ds.

XX Homo sapiens.
OS
XX US6255455-B1.
XX
XX 03-JUL-2001.
XX
XX 29-JAN-1999; 99US-00240274.
XX
XX 11-OCT-1996; 96US-0028550P.
XX
XX 27-JUN-1997; 97US-0088404S.
XX
XX 10-APR-1998; 98US-0081380P.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
XX
XX Siegel DL;
PI
XX WPI; 2001-388931/41.
XX
XX P-PSDB; AAG93644.
XX
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX
XX Example 3; Col 74; 162pp; English.
XX
XX The present invention describes an isolated Rh(D) binding protein,
CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC chain CD3 amino acid sequences which are given in the exemplification of
CC the present invention
XX
SQ Sequence 321 BP; 84 A; 89 C; 74 G; 74 T; 0 U; 0 Other;

Query Match 90.4%; Score 287.6; DB 5; Length 321;
Best Local Similarity 94.0%; Pred. No. 3.4e-81;
Matches 299; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 1 GAGCTCAGTCAGTCTCCCTCCCTGCTGTCATCTGTGGGAGACAGAGTCACCATCACT 60
DB 4 GAGCTCAGTCAGTCTCCCTCCCTGCTGTCATCTGTGGGAGACAGAGTCACCATCACT 63
QY 61 TCCCGGCAAGTCAGAGAAATTAACACCTATTAAATTGGTATCAGCATAAACAGGGAAA 120
DB 64 TCCCGGCAAGTCAGAGAAATTAACACCTATTAAATTGGTATCAGCATAAACAGGGAAA 123
QY 121 GCCCTTAAGTCTCTGATCTATGTCATCCAGTTCGAAAGTGGGTGCCATCAAGGTTTC 180
DB 124 GCCCTTAAGTCTCTGATCTATGTCATCCAGTTCGAAAGTGGGTGCCATCAAGGTTTC 183
QY 181 AGTGGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCTGAAGAT 240
DB 184 AGTGGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCTGAAGAT 243
QY 241 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCTGCTGCTACACTTTTGGCCAGGGGACC 300
DB 244 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCTGCTGCTGCTACACTTTTGGCCAGGGGACC 303
QY 301 AAGGTGGAGATCAAAACGA 318
DB 304 AAGGTGGAGATCAAAACGA 321

RESULT 3
ACD45365
ID ACD45365 standard; DNA; 321 BP.
XX

AC ACD45365;
 XX
 DT 12-SEP-2003 (first entry)
 XX
 DE Anti-Rh(D) light chain SH13 DNA.
 XX
 KW Human; ds; gene; RH(D) binding protein; blood typing; blood product;
 KW magnetically activated cell sorting.
 XX
 OS Homo sapiens.
 XX
 FN US2003040605-A1.
 XX
 PD 27-FEB-2003.
 XX
 PF 04-MAY-2001; 2001US-00848798.
 XX
 PR 11-OCT-1996; 96US-0028550P.
 XX
 PR 27-JUN-1997; 97US-00884045.
 PR 10-APR-1998; 98US-0081380P.
 PR 29-JAN-1999; 99US-00240274.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Siegel DL;
 XX
 DR WPI; 2003-512273/48.
 DR P-PSDB; ABO27451.
 XX
 PT New human Rh(D)-binding protein useful for various diagnostic and
 PT therapeutic applications, including typing of blood or blood products.
 XX
 PS Claim 12; Page 57; 187pp; English.
 XX
 CC The invention relates to an isolated Rh(D) binding protein. The protein
 CC can be used for magnetically activated cell sorting. The protein is
 CC useful in various diagnostic and therapeutic applications in humans,
 CC including typing of blood or blood products. The present sequence
 CC represents DNA encoding a human anti-Rh(D) chain
 XX
 SQ Sequence 321 BP; 84 A; 89 C; 74 G; 74 T; 0 U; 0 Other;
 Query Match 90.4%; Score 287.6; DB 8; Length 321;
 Best Local Similarity 94.0%; Pred. No. 3.4e-81;
 Matches 299; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
 QY 1 GAGCTCACTCAGTCTCCATCTCCCTGCTGTCATCTGTGGAGACAGAGTCACCATCAGT 60
 DB 4 GAGCTCACTCAGTCTCCATCTCCCTGCTGTCATCTGTGGAGACAGAGTCACCATCAGT 63
 QY 61 TGGCGGCAAGTCAGAGATTAACACCTATTAAATTGGTATCAGCATAAACCCAGGAAA 120
 DB 64 TGGCGGCAAGTCAGAGATTAACACCTATTAAATTGGTATCAGCATAAACCCAGGAAA 123
 QY 121 GCCCCTAAGCTCTCTGATCTATGCTGTCATCCAGTTTGCAAAAGTGGGTGCCATCAAGTTTC 180
 DB 124 GCCCCTAAGCTCTCTGATCTATGCTGTCATCCAGTTTGCAAAAGTGGGTGCCATCAAGTTTC 183
 QY 181 AGTGGCAGTGGATATGGGACAGACTTCACTCTCAACATCAGCAGTCTGCGACCTGAAGAT 240
 DB 184 AGTGGCAGTGGATATGGGACAGACTTCACTCTCAACATCAGCAGTCTGCGACCTGAAGAT 243
 QY 241 TTGTCAGTCTACTACTCTCAGAGAGTCTCAGTCCCTCGTACACTTTTGGCCAGGGGACC 300
 DB 244 TTGTCAGTCTACTACTCTCAGAGAGTCTCAGTCCCTCGTACACTTTTGGCCAGGGGACC 303
 QY 301 AAGGTGGAGATCAAAACGA 318
 DB 304 AAGGTGGAGATCAAAACGA 321

RESULT 4
 AAH68720

AAH68720 standard; DNA; 321 BP.
 XX
 AC AAH68720;
 XX
 DT 14-SEP-2001 (first entry)
 XX
 DE Human anti-Rh(D) antibody clone SH49 nucleotide sequence.
 XX
 KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 KW red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
 XX
 OS Homo sapiens.
 XX
 FN US6255455-B1.
 XX
 PD 03-JUL-2001.
 XX
 PF 29-JAN-1999; 99US-00240274.
 XX
 PR 11-OCT-1996; 96US-0028550P.
 PR 27-JUN-1997; 97US-00884045.
 PR 10-APR-1998; 98US-0081380P.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Siegel DL;
 XX
 DR WPI; 2001-388931/41.
 DR P-PSDB; AAG93663.
 XX
 PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine.
 XX
 PS Example 3; Col 79; 162pp; English.
 XX
 CC The present invention describes an isolated Rh(D) binding protein.
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification of
 CC the present invention
 XX
 SQ Sequence 321 BP; 85 A; 87 C; 77 G; 72 T; 0 U; 0 Other;
 Query Match 88.4%; Score 281.2; DB 5; Length 321;
 Best Local Similarity 92.8%; Pred. No. 3.7e-79;
 Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
 QY 1 GAGTCATCTCAGTCTCCATCTCCCTGCTGTCATCTGTGGAGACAGAGTCACCATCAGT 60
 DB 4 GAGTCATCTCAGTCTCCATCTCCCTGCTGTCATCTGTGGAGACAGAGTCACCATCAGT 63
 QY 61 TGGCGGCAAGTCAGAGATTAACACCTATTAAATTGGTATCAGCATAAACCCAGGAAA 120
 DB 64 TGGCGGCAAGTCAGAGATTAACACCTATTAAATTGGTATCAGCATAAACCCAGGAAA 123
 QY 121 GCCCCTAAGCTCTCTGATCTATGCTGTCATCCAGTTTGCAAAAGTGGGTGCCATCAAGTTTC 180
 DB 124 GCCCCTAAGCTCTCTGATCTATGCTGTCATCCAGTTTGCAAAAGTGGGTGCCATCAAGTTTC 183
 QY 181 AGTGGCAGTGGATATGGGACAGACTTCACTCTCAACATCAGCAGTCTGCGACCTGAAGAT 240
 DB 184 AGTGGCAGTGGATATGGGACAGACTTCACTCTCAACATCAGCAGTCTGCGACCTGAAGAT 243
 QY 241 TTGTCAGTCTACTACTCTCAGAGAGTCTCAGTCCCTCGTACACTTTTGGCCAGGGGACC 300
 DB 244 TTGTCAGTCTACTACTCTCAGAGAGTCTCAGTCCCTCGTACACTTTTGGCCAGGGGACC 303

QY 301 AAGTGGAGATCAACGA 318
 DB 304 AAGTGGAAATCAACGA 321

RESULT 5

AAH68654
 ID AAH68654 standard; DNA; 321 BP.

XX AC AAH68654;
 XX DT 14-SEP-2001 (first entry)
 XX DE Human anti-Rh(D) chain I09 nucleotide sequence.

XX KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 XX KW red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
 XX OS Homo sapiens.

XX PN US255455-B1.

XX PD 03-JUL-2001.

XX PF 29-JAN-1999; 99US-00240274.

XX PR 11-OCT-1996; 96US-0028550P.

XX PR 27-JUN-1997; 97US-00884045.

XX PR 10-APR-1998; 98US-0081380P.

XX PA (UYPE-) UNIV PENNSYLVANIA.

XX PI Siegel DL;

XX DR WPI; 2001-388931/41.

XX DR P-PSDB; AAG93597.

XX PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine.
 XX PS Example 2; Col 56; 162pp; English.

XX CC The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification of
 CC the present invention

XX SQ Sequence 321 BP; 85 A; 87 C; 73 G; 76 T; 0 U; 0 Other;

Query Match 88.4%; Score 281.2; DB 5; Length 321;
 Best Local Similarity 92.8%; Pred. No. 3.7e-79;
 Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 GAGCTCACTCACTCCCTCCCTGCTGCTGATCTGTGGGAGACAGAGTCCACATCACT 60
 DB 4 GAGTCACCCAGTCTCCATCCCTCCCTGCTGCTGATCTGTGGGAGACAGAGTCCACATCACT 63

QY 61 TGCCTGGGAGTCAAGATTAACACCTATTAAATTTGATATCAGCATAAACAGGGAAA 120

DB 64 TGCCTGGGAGTCAAGATTAACACCTATTAAATTTGATATCAGCATAAACAGGGAAA 123

QY 121 GCGCCCTAAGCTCTGATCTATGCTGATCCATTTGCAAGTGGGGTCCATCAAGTTTC 180

DB 124 GCGCCCTAAGCTCTGATCTATGCTGATCCATTTGCAAGTGGGGTCCATCAAGTTTC 183

QY 181 AGTGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCTCAAGAT 240
 DB 184 AGTGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCTCAAGAT 243
 QY 241 TTTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGACC 300
 DB 244 TTTGCAACTTATTACTGTCAACAGCTTAATAGTTACCGGTACACTTTTGGCCAGGGACC 303
 QY 301 AAGTGGAGATCAACGA 318
 DB 304 AAGCTGGAGATCAACGA 321

RESULT 6

AAH68647

ID AAH68647 standard; DNA; 321 BP.

XX AC AAH68647;

XX DT 14-SEP-2001 (first entry)

XX DE Human anti-Rh(D) chain I02 nucleotide sequence.

XX KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 XX KW red blood cell; Rh phenotype; diagnosis; therapeutic; ds.

XX OS Homo sapiens.

XX PN US255455-B1.

XX PD 03-JUL-2001.

XX PF 29-JAN-1999; 99US-00240274.

XX PR 11-OCT-1996; 96US-0028550P.

XX PR 27-JUN-1997; 97US-00884045.

XX PR 10-APR-1998; 98US-0081380P.

XX PA (UYPE-) UNIV PENNSYLVANIA.

XX PI Siegel DL;

XX DR WPI; 2001-388931/41.

XX DR P-PSDB; AAG93590.

XX PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine.
 XX PS Example 2; Col 54; 162pp; English.

XX CC The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification of
 CC the present invention

XX SQ Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;

Query Match 88.4%; Score 281.2; DB 5; Length 321;
 Best Local Similarity 92.8%; Pred. No. 3.7e-79;
 Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 GAGCTCACTCACTCCCTCCCTGCTGCTGATCTGTGGGAGACAGAGTCCACATCACT 60

DB 4 GAGCTCACTCACTCCCTCCCTGCTGCTGATCTGTGGGAGACAGAGTCCACATCACT 63

QY 61 TGCGGGCAAGTCAGAGATTAAACACCTATTATTAATTTGGTATCAGATAAACCCAGGAAA 120
 DB 64 TGCGGGCAAGTCAGAGATTAAACACCTATTATTAATTTGGTATCAGATAAACCCAGGAAA 123
 QY 121 GCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTT 180
 DB 124 GCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTT 183
 QY 181 AGTGGCAGTGATATGGACAGACTTCACTCTCACCATCAGAGTCTCGAGCCTGAAGAT 240
 DB 184 AGTGGCAGTGATATGGACAGACTTCACTCTCACCATCAGAGTCTCGAGCCTGAAGAT 243
 QY 241 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGTACACTTTTGGCCAGGGACC 300
 DB 244 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGTACACTTTTGGCCAGGGACC 303
 QY 301 AAGGTGGAGATCAACGA 318
 DB 304 AAGGTGGAAATCAACGA 321

RESULT 7

ACD45311
 ID ACD45311 standard; DNA; 321 BP.

XX AC ACD45311;

DT 12-SEP-2003 (first entry)

XX DE Anti-Rh(D) chain I02 DNA.

XX KW Human; ds; gene; RH(D) binding protein; blood typing; blood product;
 XX KM magnetically activated cell sorting.

XX OS Homo sapiens.

XX PN US2003040605-A1.

XX PD 27-FEB-2003.

XX PF 04-MAY-2001; 2001US-00848798.

XX PR 11-OCT-1996; 96US-0028550P.

XX PR 27-JUN-1997; 97US-00884045.

XX PR 10-APR-1998; 98US-0081380P.

XX PR 29-JAN-1999; 99US-00240274.

XX PA (UYPE-) UNIV PENNSYLVANIA.

XX PI Siegel DL;

XX DR WPI; 2003-512273/48.

XX DR P-PSDB; ABO27397.

XX PT New human Rh(D)-binding protein useful for various diagnostic and
 XX PT therapeutic applications, including typing of blood or blood products.

XX PS Claim 12; Page 39; 187pp; English.

XX CC The invention relates to an isolated Rh(D) binding protein. The protein
 XX CC can be used for magnetically activated cell sorting. The protein is
 XX CC useful in various diagnostic and therapeutic applications in humans,
 XX CC including typing of blood or blood products. The present sequence
 XX CC represents DNA encoding a human anti-Rh(D) chain

XX SQ Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;

Query Match 88.4%; Score 281.2; DB 8; Length 321;

Best Local Similarity 92.8%; Pred. No. 3.7e-79;

Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 GAGTCACTCAGTCTCCATCTCCTGCTGATCTGTGGAGAGAGTCAACCATCAGT 60

DB 4 GAGTCACTCAGTCTCCTGCTGATCTGTAGGAGACAGAGTCAACCATCAGT 63
 QY 61 TGCGGGCAAGTCAGAGATTAAACACCTATTATTAATTTGGTATCAGATAAACCCAGGAAA 120
 DB 64 TGCGGGCAAGTCAGAGATTAAACACCTATTATTAATTTGGTATCAGATAAACCCAGGAAA 123
 QY 121 GCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTT 180
 DB 124 GCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTT 183
 QY 181 AGTGGCAGTGATATGGACAGACTTCACTCTCACCATCAGAGTCTCGAGCCTGAAGAT 240
 DB 184 AGTGGCAGTGATATGGACAGACTTCACTCTCACCATCAGAGTCTCGAGCCTGAAGAT 243
 QY 241 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGTACACTTTTGGCCAGGGACC 300
 DB 244 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGTACACTTTTGGCCAGGGACC 303
 QY 301 AAGGTGGAGATCAACGA 318
 DB 304 AAGGTGGAAATCAACGA 321

RESULT 8

ACD45318
 ID ACD45318 standard; DNA; 321 BP.

XX AC ACD45318;

DT 12-SEP-2003 (first entry)

XX DE Anti-Rh(D) chain I09 DNA.

XX KW Human; ds; gene; RH(D) binding protein; blood typing; blood product;
 XX KM magnetically activated cell sorting.

XX OS Homo sapiens.

XX PN US2003040605-A1.

XX PD 27-FEB-2003.

XX PF 04-MAY-2001; 2001US-00848798.

XX PR 11-OCT-1996; 96US-0028550P.

XX PR 27-JUN-1997; 97US-00884045.

XX PR 10-APR-1998; 98US-0081380P.

XX PR 29-JAN-1999; 99US-00240274.

XX PA (UYPE-) UNIV PENNSYLVANIA.

XX PI Siegel DL;

XX DR WPI; 2003-512273/48.

XX DR P-PSDB; ABO27404.

XX PT New human Rh(D)-binding protein useful for various diagnostic and
 XX PT therapeutic applications, including typing of blood or blood products.

XX PS Claim 12; Page 41; 187pp; English.

XX CC The invention relates to an isolated Rh(D) binding protein. The protein
 XX CC can be used for magnetically activated cell sorting. The protein is
 XX CC useful in various diagnostic and therapeutic applications in humans,
 XX CC including typing of blood or blood products. The present sequence
 XX CC represents DNA encoding a human anti-Rh(D) chain

XX SQ Sequence 321 BP; 85 A; 87 C; 73 G; 76 T; 0 U; 0 Other;

Query Match 88.4%; Score 281.2; DB 8; Length 321;

Best Local Similarity 92.8%; Pred. No. 3.7e-79;

Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 GAGCTCAGTCTCCATCCCTCCCTGTCATCTGTGGGAGACAGAGTCACCATCACT 60
DB 4 GAGCTCACCCAGTCTCCATCCCTCCCTGTCATCTGTAGGAGACAGAGTCACCATCACT 63
QY 61 TCCCGGGCAAGTCAGAGAAATTAACACCTATTAAATTTGGTATCAGCATAAACCCAGGAAA 120
DB 64 TCCCGGGCAAGTCAGAGAAATTAACACCTATTAAATTTGGTATCAGCATAAACCCAGGAAA 123
QY 121 GCCCTTAAGCTCCTGATCTATGCTGATCCAGTATTGCAAGTGGGGTCCCATCAAGGTTTC 180
DB 124 GCCCTTAAGCTCCTGATCTATGCTGATCCAGTATTGCAAGTGGGGTCCCATCAAGGTTTC 183
QY 181 AGTGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCCTGAAGAT 240
DB 184 AGTGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCCTGAAGAT 243
QY 241 TTTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGACC 300
DB 244 TTTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGACC 303
QY 301 AAGTGGAGATCAAAACGA 318
DB 304 AAGTGGAGATCAAAACGA 321

RESULT 9
ACD45384
ID ACD45384 standard; DNA; 321 BP.
AC ACD45384;
XX
DT 12-SEP-2003 (first entry)
XX
DE Anti-Rh(D) light chain SH49 DNA.
XX
KW Human; ds; gene; RH(D) binding protein; blood typing; blood product;
KW magnetically activated cell sorting.
XX
OS Homo sapiens.
XX
PN US2003040605-A1.
XX
PD 27-FEB-2003.
XX
PF 04-MAY-2001; 2001US-00848798.
XX
PR 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-00884045.
PR 10-APR-1998; 98US-0081380P.
PR 29-JAN-1999; 99US-00240274.
XX
PA (TYPE-) UNIV PENNSYLVANIA.
XX
PI Siegel DL;
XX
WPI; 2003-512273/48.
DR P-PSDB; ABO27470.
XX
PT New human Rh(D)-binding protein useful for various diagnostic and
PT therapeutic applications, including typing of blood or blood products.
PS
PS Claim 12; Page 61; 187pp; English.
XX
CC The invention relates to an isolated Rh(D) binding protein. The protein
CC can be used for magnetically activated cell sorting. The protein is
CC useful in various diagnostic and therapeutic applications in humans,
CC including typing of blood or blood products. The present sequence
CC represents DNA encoding a human anti-Rh(D) chain
XX
SQ Sequence 321 BP; 85 A; 87 C; 77 G; 72 T; 0 U; 0 Other;

Query Match 88.4%; Score 281.2; DB 8; Length 321;

Best Local Similarity 92.8%; Pred. No. 3.7e-79;
Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 1 GAGCTCAGTCTCCATCCCTCCCTGTCATCTGTGGGAGACAGAGTCACCATCACT 60
DB 4 GAGCTCACCCAGTCTCCATCCCTCCCTGTCATCTGTAGGAGACAGAGTCACCATCACT 63
QY 61 TCCCGGGCAAGTCAGAGAAATTAACACCTATTAAATTTGGTATCAGCATAAACCCAGGAAA 120
DB 64 TCCCGGGCAAGTCAGAGAAATTAACACCTATTAAATTTGGTATCAGCATAAACCCAGGAAA 123
QY 121 GCCCTTAAGCTCCTGATCTATGCTGATCCAGTATTGCAAGTGGGGTCCCATCAAGGTTTC 180
DB 124 GCCCTTAAGCTCCTGATCTATGCTGATCCAGTATTGCAAGTGGGGTCCCATCAAGGTTTC 183
QY 181 AGTGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCCTGAAGAT 240
DB 184 AGTGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCCTGAAGAT 243
QY 241 TTTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGACC 300
DB 244 TTTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGACC 303
QY 301 AAGTGGAGATCAAAACGA 318
DB 304 AAGTGGAGATCAAAACGA 321

RESULT 10
AAT66781
ID AAT66781 standard; cDNA; 321 BP.
AC AAT66781;
XX
DT 29-JAN-1998 (first entry)
XX
DE Anti-cancer specific antigen MAb light chain variable region cDNA.
XX
KW Light chain; variable region; cancer specific antigen; human;
KW monoclonal antibody; hMAb; diagnosis; cancer; immunotherapy;
KW purification; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT mat_peptide 1..321
FT /tag= a
XX
XX JP09098786-A.
XX
XX 15-APR-1997.
XX
PF 06-OCT-1995; 95JP-00284400.
XX
PR 06-OCT-1995; 95JP-00284400.
XX
PA (MOMI) MORINAGA & CO LTD.
PA (SHKJ) SHINGIJUTSU JIGYODAN.
XX
WPI; 1997-275445/25.
DR P-PSDB; AAW16649.
XX
PT cDNA encoding human monoclonal antibody - useful in medicine, or to
PT purify cancer specific antigen.
PS Claim 2; Fig 2; 7pp; Japanese.
XX
CC The present sequence encodes the light chain variable region of an anti-
CC cancer specific antigen human monoclonal antibody (hMAb). The hMAb can be
CC used in medicine, e.g. clinical diagnosis of cancer or immunotherapy, or
CC to purify cancer specific antigen. The industrial scale production of
CC large amounts of the hMAb is made feasible by genetic engineering using
CC the hMAb cDNA

PD 03-JUL-2001.
 XX
 XX 29-JAN-1999; 99US-00240274.
 XX
 XX 11-OCT-1996; 96US-0028550P.
 PR 27-JUN-1997; 97US-00884045.
 PR 10-APR-1998; 98US-0081380P.
 XX
 XX (UYPE-) UNIV PENNSYLVANIA.
 PA
 XX Siegel DL;
 PI
 XX WPI; 2001-388931/41.
 DR P-PSDB; AAG93595.
 XX
 XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine.
 XX
 XX Example 2; Col 55; 162pp; English.
 PS
 XX The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification of
 CC the present invention
 XX
 XX Sequence 321 BP; 85 A; 87 C; 76 G; 73 T; 0 U; 0 Other;

Query Match 87.9%; Score 279.6; DB 5; Length 321;
 Best Local Similarity 92.5%; Pred. No. 1.2e-78;
 Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
 QY 1 GAGTCACTCAGTCTCCATCTCCTGCTGTCATCTGTGGAGACAGAGTCACCATCAGT 60
 Db 4 GAGTCACTCAGTCTCCATCTCCTGCTGTCATCTGTGGAGACAGAGTCACCATCAGT 63
 QY 61 TGCCGGGCAAGTCAGAGATTAACACCTATTAAATTGGTATCAGCATTAACACAGGAAA 120
 Db 64 TGCCGGGCAAGTCAGAGATTAACACCTATTAAATTGGTATCAGCATTAACACAGGAAA 123
 QY 121 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAGTGGGGTCCCATCAAGGTTT 180
 Db 124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAGTGGGGTCCCATCAAGGTTT 183
 QY 181 AGTGGCAGTGGATATGGACAGACTTCACCTCACCATCAGCAGTCTGCAGCCTGAAGAT 240
 Db 184 AGTGGCAGTGGATATGGACAGACTTCACCTCACCATCAGCAGTCTGCAGCCTGAAGAT 243
 QY 241 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTCCCTGCTACACTTTTGGCCAGGGGACC 300
 Db 244 TTGCAACTTACTACTGTCAAGAGAGTCTCAGTCCCTGCTACACTTTTGGCCAGGGGACC 303
 QY 301 AAGGTGAGATCAACGA 318
 Db 304 AAGGTGAGATCAACGA 321

RESULT 15
 ACD45388
 ID ACD45388 standard; DNA; 321 BP.
 AC ACD45388;
 XX
 XX 12-SEP-2003 (first entry)
 XX
 XX Anti-Rh(D) light chain SH54 DNA.

XX Human; ds; gene; RH(D) binding protein; blood typing; blood product;
 KW magnetically activated cell sorting.
 XX
 XX Homo sapiens.
 XX
 XX US2003040605-A1.
 XX
 XX 27-FEB-2003.
 XX
 XX 04-MAY-2001; 2001US-00848798.
 XX
 XX 11-OCT-1996; 96US-0028550P.
 PR 27-JUN-1997; 97US-00884045.
 PR 10-APR-1998; 98US-0081380P.
 PR 29-JAN-1999; 99US-00240274.
 XX
 XX (UYPE-) UNIV PENNSYLVANIA.
 PA
 XX Siegel DL;
 PI
 XX WPI; 2003-512273/48.
 DR P-PSDB; ABO27474.
 XX
 XX New human Rh(D)-binding protein useful for various diagnostic and
 PT therapeutic applications, including typing of blood or blood products.
 XX
 XX Claim 12; Page 61; 187pp; English.
 PS
 XX The invention relates to an isolated Rh(D) binding protein. The protein
 CC can be used for magnetically activated cell sorting. The protein is
 CC useful in various diagnostic and therapeutic applications in humans,
 CC including typing of blood or blood products. The present sequence
 CC represents DNA encoding a human anti-Rh(D) chain
 XX
 XX Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;

Query Match 87.9%; Score 279.6; DB 8; Length 321;
 Best Local Similarity 92.5%; Pred. No. 1.2e-78;
 Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
 QY 1 GAGTCACTCAGTCTCCATCTCCTGCTGTCATCTGTGGAGACAGAGTCACCATCAGT 60
 Db 4 GAGTCACTCAGTCTCCATCTCCTGCTGTCATCTGTGGAGACAGAGTCACCATCAGT 63
 QY 61 TGCCGGGCAAGTCAGAGATTAACACCTATTAAATTGGTATCAGCATTAACACAGGAAA 120
 Db 64 TGCCGGGCAAGTCAGAGATTAACACCTATTAAATTGGTATCAGCATTAACACAGGAAA 123
 QY 121 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAGTGGGGTCCCATCAAGGTTT 180
 Db 124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAGTGGGGTCCCATCAAGGTTT 183
 QY 181 AGTGGCAGTGGATATGGACAGACTTCACCTCACCATCAGCAGTCTGCAGCCTGAAGAT 240
 Db 184 AGTGGCAGTGGATATGGACAGACTTCACCTCACCATCAGCAGTCTGCAGCCTGAAGAT 243
 QY 241 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTCCCTGCTACACTTTTGGCCAGGGGACC 300
 Db 244 TTGCAACTTACTACTGTCAAGAGAGTCTCAGTCCCTGCTACACTTTTGGCCAGGGGACC 303
 QY 301 AAGGTGAGATCAACGA 318
 Db 304 AAGGTGAGATCAACGA 321

Search completed: August 13, 2004, 01:35:52
 Job time : 209.182 secs

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OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 03:58:10 ; Search time 706.827 Seconds
(without alignments)
2207.472 Million cell updates/sec

Title: US-10-027-725A-4

Perfect score: 318

Sequence: 1 gagctcactcagctccatc.....ccaaagtggagatcaaacga 318

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3225727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters: 6451454

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
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5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
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8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2.*
14: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	318	100.0	318	15	US-10-027-725A-4
2	287.6	90.4	321	10	US-09-848-798-199
3	281.2	88.4	321	10	US-09-848-798-102
4	281.2	88.4	321	10	US-09-848-798-109
5	281.2	88.4	321	10	US-09-848-798-218
6	279.6	87.9	321	10	US-09-848-798-107
7	279.6	87.9	321	10	US-09-848-798-113
8	279.6	87.9	321	10	US-09-848-798-221
9	279.6	87.9	321	10	US-09-848-798-222
10	277.6	87.3	324	17	US-10-344-514-3
11	277.6	87.3	324	17	US-10-344-514-4
12	277.6	87.3	333	15	US-10-203-754A-60
13	277.6	87.3	900	15	US-10-203-754A-64
14	276.4	86.9	321	10	US-09-848-798-201

15	276.4	86.9	321	10	US-09-848-798-211	Sequence 211, App
16	276.2	86.9	324	10	US-09-848-798-101	Sequence 101, App
17	276.2	86.9	324	10	US-09-848-798-112	Sequence 112, App
18	276.2	86.9	324	10	US-09-848-798-210	Sequence 210, App
19	276	86.8	720	9	US-09-192-854-1	Sequence 1, Appli
20	276	86.8	720	9	US-09-968-561A-1	Sequence 1, Appli
21	276	86.8	720	10	US-09-968-744A-1	Sequence 1, Appli
22	276	86.8	720	13	US-09-968-561A-1	Sequence 1, Appli
23	275.4	86.6	729	15	US-10-216-484-125	Sequence 125, App
24	275.4	86.6	729	15	US-10-384-933-125	Sequence 125, App
25	274.8	86.4	321	10	US-09-848-798-105	Sequence 105, App
26	274.8	86.4	321	10	US-09-848-798-216	Sequence 216, App
27	274.2	86.2	322	17	US-10-038-591-54	Sequence 54, Appl
28	273.8	86.1	333	15	US-10-203-754A-61	Sequence 61, Appl
29	273.8	86.1	900	15	US-10-203-754A-65	Sequence 65, Appl
30	273.2	85.9	321	10	US-09-848-798-104	Sequence 104, App
31	273.2	85.9	321	10	US-09-848-798-106	Sequence 106, App
32	273.2	85.9	321	10	US-09-848-798-215	Sequence 215, App
33	273.2	85.9	321	10	US-09-848-798-217	Sequence 217, App
34	273	85.8	324	10	US-09-848-798-206	Sequence 206, App
35	271.8	85.5	322	16	US-10-309-762-226	Sequence 226, App
36	271.8	85.5	322	16	US-10-309-762-227	Sequence 227, App
37	271.4	85.3	324	10	US-09-848-798-110	Sequence 110, App
38	270.6	85.1	714	15	US-10-153-382-18	Sequence 18, Appl
39	270.6	85.1	1106	16	US-10-264-049-121	Sequence 121, App
40	270.2	85.0	322	16	US-10-309-762-231	Sequence 231, App
41	270.2	85.0	322	16	US-10-309-762-233	Sequence 233, App
42	270	84.9	321	10	US-09-848-798-205	Sequence 205, App
43	270	84.9	321	10	US-09-848-798-207	Sequence 207, App
44	269.6	84.8	324	17	US-10-344-514-7	Sequence 7, Appli
45	269.6	84.8	324	17	US-10-344-514-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-10-027-725A-4
; Sequence 4, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 318
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-027-725A-4

Query Match 100.0%; Score 318; DB 15; Length 318;
Best Local Similarity 100.0%; Pred. No. 4.1e-97;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GAGCTCAGTCTCCATCCCTCCCTGCTGATCTGTGGGACAGAGTCCATCAGT	60
Db	1	GAGCTCAGTCTCCATCCCTCCCTGCTGATCTGTGGGACAGAGTCCATCAGT	60
QY	61	TGCGGGCAAGTCAGAGATTAACTATTAAATTTGATATCAGCATAAACCGGAAA	120
Db	61	TGCGGGCAAGTCAGAGATTAACTATTAAATTTGATATCAGCATAAACCGGAAA	120
QY	121	GCCCCTAAGTCTCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGTCCCATCAAGTTTC	180
Db	121	GCCCCTAAGTCTCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGTCCCATCAAGTTTC	180
QY	181	AGTGGCAGTGGATATGGGACAGACTTCTCTCAATCAGCAGTCTGCAGCCTGAAGAT	240

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Db 181 ATGGCAGTGGATGAGCAGAGCTTCACTCTCACCATCAGCAGCTGTCAGCCTGAAGAT 240
Qy 241 TTTCGAAGTACTACTGTCAGAGAGTCTCAGTCCCTCGTACACTTTTGCCAGGGGACC 300
Db 241 TTTCGAAGTACTACTGTCAGAGAGTCTCAGTCCCTCGTACACTTTTGCCAGGGGACC 300
Qy 301 AAGGTGGAGATCAAAACGA 318
Db 301 AAGGTGGAGATCAAAACGA 318

RESULT 2
US-09-848-798-199
; Sequence 199, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-01-29
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-01-29
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 199
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-848-798-199
Query Match 90.4%; Score 287.6; DB 10; Length 321;
Best Local Similarity 94.0%; Pred. No. 8.2e-87; Indels 0; Gaps 0;
Matches 299; Conservative 0; Mismatches 19;

Qy 1 GAGCTCACTAGTCTCCATCCCTCGTCTGATCTGCGAGAGAGTCCCATCAGT 60
Db 4 GAGCTCACCAGTCTCCATCCCTCGTCTGATCTGCGAGAGAGTCCCATCAGT 63
Qy 61 TCCCGGCAAGTCAGAGAAATTAACACCTATTAAATTTGGTATCAGCATAAACCCAGGAAA 120
Db 64 TCCCGGCAAGTCAGAGAAATTAACACCTATTAAATTTGGTATCAGCATAAACCCAGGAAA 123
Qy 121 GCCCTTAAGTCTCTGATCTATGTCGATTCAGTGGATTTGAAAAGTGGGTCCTCAAGGTTTC 180
Db 124 GCCCTTAAGTCTCTGATCTATGTCGATTCAGTGGATTTGAAAAGTGGGTCCTCAAGGTTTC 183
Qy 181 AGTGCAGTGGATATGGAGACAGTCTCACTCTCACCATCAGCAGTCTGCAGCCTGAAGAT 240
Db 184 AGTGCAGTGGATATGGAGACAGTCTCACTCTCACCATCAGCAGTCTGCAGCCTGAAGAT 243
Qy 241 TTTCGAAGTACTACTGTCAGAGAGTCTCAGTCCCTCGTACACTTTTGCCAGGGGACC 300
Db 244 TTTCGAAGTACTACTGTCAGAGAGTCTCAGTCCCTCGTACACTTTTGCCAGGGGACC 303
Qy 301 AAGGTGGAGATCAAAACGA 318
Db 304 AAGGTGGAGATCAAAACGA 321

RESULT 3
US-09-848-798-102
; Sequence 102, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-01-29
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-01-29
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 109
US-09-848-798-102
Query Match 88.4%; Score 281.2; DB 10; Length 321;
```

```
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-01-29
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-01-29
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 102
US-09-848-798-102
Query Match 88.4%; Score 281.2; DB 10; Length 321;
Best Local Similarity 92.8%; Pred. No. 1.2e-84;
Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 1 GAGCTCACTAGTCTCCATCCCTCGTCTGATCTGCGAGAGAGTCCCATCAGT 60
Db 4 GAGCTCACCAGTCTCCATCCCTCGTCTGATCTGCGAGAGAGTCCCATCAGT 63
Qy 61 TCCCGGCAAGTCAGAGAAATTAACACCTATTAAATTTGGTATCAGCATAAACCCAGGAAA 120
Db 64 TCCCGGCAAGTCAGAGAAATTAACACCTATTAAATTTGGTATCAGCATAAACCCAGGAAA 123
Qy 121 GCCCTTAAGTCTCTGATCTATGTCGATTCAGTGGATTTGAAAAGTGGGTCCTCAAGGTTTC 180
Db 124 GCCCTTAAGTCTCTGATCTATGTCGATTCAGTGGATTTGAAAAGTGGGTCCTCAAGGTTTC 183
Qy 181 AGTGCAGTGGATATGGAGACAGTCTCACTCTCACCATCAGCAGTCTGCAGCCTGAAGAT 240
Db 184 AGTGCAGTGGATATGGAGACAGTCTCACTCTCACCATCAGCAGTCTGCAGCCTGAAGAT 243
Qy 241 TTTCGAAGTACTACTGTCAGAGAGTCTCAGTCCCTCGTACACTTTTGCCAGGGGACC 300
Db 244 TTTCGAAGTACTACTGTCAGAGAGTCTCAGTCCCTCGTACACTTTTGCCAGGGGACC 303
Qy 301 AAGGTGGAGATCAAAACGA 318
Db 304 AAGGTGGAGATCAAAACGA 321

RESULT 4
US-09-848-798-109
; Sequence 109, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-01-29
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-01-29
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 109
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 109
US-09-848-798-109
Query Match 88.4%; Score 281.2; DB 10; Length 321;
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; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 113
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain II3
US-09-848-798-113

Query Match      87.9%; Score 279.6; DB 10; Length 321;
Best Local Similarity 92.5%; Pred. No. 4.2e-84;
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 GAGCTCACTCAGTCTCCATCCTCCTGCTGCACTCTGCGGAGACAGAGTCACCATCAGT 60
Db 4 GAGCTCACTCAGTCTCCATCCTCCTGCTGCACTCTGCGGAGACAGAGTCACCATCAGT 63

QY 61 TCCCGGCAAGTCAGAGAAATAACACCTATTAAATTTGGTATCAGCATAAACACCGGAAA 120
Db 64 TCCCGGCAAGTCAGAGCAATGGCACATTATTTAAATTTGGTATCAGCAGAAACCGGAAA 123

QY 121 GCCCTTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTTC 180
Db 124 GCCCTTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTTC 183

QY 181 AGTGGCAGTGGATATGGACAGAGCTTCACTCTCCACATCAGAGCTCTGCAGCCTGAAGAT 240
Db 184 AGTGGCAGTGGATCTGGACAGAGTTTCACTCTCCACATCAGAGCTCTGCACCTGAAGAT 243

QY 241 TTTGCAAGTTACTACTCTCAGAGAGTCTCAGTCGCTGCTACACTTTTGGCCAGGGGACC 300
Db 244 TTTGCAAGTTACTACTCTCAGAGAGTCTCAGTCGCTGCTACACTTTTGGCCAGGGGACC 303

QY 301 AAGGTGGAGATCAAAACGA 318
Db 304 AAGGTGGAGATCAAAACGA 321

RESULT 9
US-09-848-798-222
; Sequence 222, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 222
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-848-798-222

Query Match      87.9%; Score 279.6; DB 10; Length 321;
Best Local Similarity 92.5%; Pred. No. 4.2e-84;
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 GAGCTCACTCAGTCTCCATCCTCCTGCTGCACTCTGCGGAGACAGAGTCACCATCAGT 60
Db 4 GAGCTCACTCAGTCTCCATCCTCCTGCTGCACTCTGCGGAGACAGAGTCACCATCAGT 63

QY 61 TCCCGGCAAGTCAGAGAAATAACACCTATTAAATTTGGTATCAGCATAAACACCGGAAA 120
Db 64 TCCCGGCAAGTCAGAGCAATGGCACATTATTTAAATTTGGTATCAGCAGAAACCGGAAA 123

QY 121 GCCCTTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTTC 180
Db 124 GCCCTTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTTC 183

QY 181 AGTGGCAGTGGATATGGACAGAGCTTCACTCTCCACATCAGAGCTCTGCAGCCTGAAGAT 240
Db 184 AGTGGCAGTGGATCTGGACAGAGTTTCACTCTCCACATCAGAGCTCTGCACCTGAAGAT 243

QY 241 TTTGCAAGTTACTACTCTCAGAGAGTCTCAGTCGCTGCTACACTTTTGGCCAGGGGACC 300
Db 244 TTTGCAAGTTACTACTCTCAGAGAGTCTCAGTCGCTGCTACACTTTTGGCCAGGGGACC 303

QY 301 AAGGTGGAGATCAAAACGA 318
Db 304 AAGGTGGAGATCAAAACGA 321
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; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 113
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain II3
US-09-848-798-113

Query Match      87.9%; Score 279.6; DB 10; Length 321;
Best Local Similarity 92.5%; Pred. No. 4.2e-84;
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 GAGCTCACTCAGTCTCCATCCTCCTGCTGCACTCTGCGGAGACAGAGTCACCATCAGT 60
Db 4 GAGCTCACTCAGTCTCCATCCTCCTGCTGCACTCTGCGGAGACAGAGTCACCATCAGT 63

QY 61 TCCCGGCAAGTCAGAGAAATAACACCTATTAAATTTGGTATCAGCATAAACACCGGAAA 120
Db 64 TCCCGGCAAGTCAGAGCAATGGCACATTATTTAAATTTGGTATCAGCAGAAACCGGAAA 123

QY 121 GCCCTTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTTC 180
Db 124 GCCCTTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTTC 183

QY 181 AGTGGCAGTGGATATGGACAGAGCTTCACTCTCCACATCAGAGCTCTGCAGCCTGAAGAT 240
Db 184 AGTGGCAGTGGATCTGGACAGAGTTTCACTCTCCACATCAGAGCTCTGCACCTGAAGAT 243

QY 241 TTTGCAAGTTACTACTCTCAGAGAGTCTCAGTCGCTGCTACACTTTTGGCCAGGGGACC 300
Db 244 TTTGCAAGTTACTACTCTCAGAGAGTCTCAGTCGCTGCTACACTTTTGGCCAGGGGACC 303

QY 301 AAGGTGGAGATCAAAACGA 318
Db 304 AAGGTGGAGATCAAAACGA 321

RESULT 8
US-09-848-798-221
; Sequence 221, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 221
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH52
US-09-848-798-221

Query Match      87.9%; Score 279.6; DB 10; Length 321;
Best Local Similarity 92.5%; Pred. No. 4.2e-84;
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 GAGCTCACTCAGTCTCCATCCTCCTGCTGCACTCTGCGGAGACAGAGTCACCATCAGT 60
Db 4 GAGCTCACTCAGTCTCCATCCTCCTGCTGCACTCTGCGGAGACAGAGTCACCATCAGT 63

QY 61 TCCCGGCAAGTCAGAGAAATAACACCTATTAAATTTGGTATCAGCATAAACACCGGAAA 120
Db 64 TCCCGGCAAGTCAGAGCAATGGCACATTATTTAAATTTGGTATCAGCAGAAACCGGAAA 123

QY 121 GCCCTTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTTC 180
Db 124 GCCCTTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTTC 183

QY 181 AGTGGCAGTGGATATGGACAGAGCTTCACTCTCCACATCAGAGCTCTGCAGCCTGAAGAT 240
Db 184 AGTGGCAGTGGATCTGGACAGAGTTTCACTCTCCACATCAGAGCTCTGCACCTGAAGAT 243

QY 241 TTTGCAAGTTACTACTCTCAGAGAGTCTCAGTCGCTGCTACACTTTTGGCCAGGGGACC 300
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QY 301 AAGGTGGAGATCAAAACGA 318
Db 304 AAGGTGGAGATCAAAACGA 321
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QY 182 GTGCAGTGGATATGGACAGATTCCTCTCAACATCAGCAGTCTGCAGCTGAAGATT 241
DB 188 GTGCAGTGGATCTGGACAGATTCCTCTCAACATCAGCAGTCTGAACCTGAAGATT 247
QY 242 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCTGTAACATTTTGGCCAGGGGACCA 301
DB 248 TTGCAACTTACTACTGTCAAGAGAGTCTCAGTGCCTCTGTAACATTTTGGCCAGGGGACCA 307
QY 302 AGGTGGAGATCAACG 317
DB 308 AGGTGGAGATCAACG 323

RESULT 13
US-10-203-754A-64
; Sequence 64, Application US/10203754A
; Publication No. US20030157132A1
; GENERAL INFORMATION:
; APPLICANT: ITAMI, Seima
; APPLICANT: SEKI, Makoto
; APPLICANT: MATSUURA, Yoshiharu
; APPLICANT: SHIBUI, Tatsuro
; APPLICANT: YOTSUMOTO, Yoshihisa
; APPLICANT: MIYAMURA, Tatsuo
; TITLE OF INVENTION: Therapeutic Agent for Hepatitis C
; FILE REFERENCE: P22257
; CURRENT APPLICATION NUMBER: US/10/203,754A
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/JP01/00967
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 900
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-203-754A-64

Query Match 87.3%; Score 277.6; DB 15; Length 900;
Best Local Similarity 92.4%; Pred. No. 38-83; Indels 0; Gaps 0;
Matches 292; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 2 AGTCACTCAGTCTCCATCCCTGCTGCACTCTGTGGAGACAGATCCACATCAGTT 61
DB 503 AGATGACCCAGTCTCCATCCCTGCTGCACTCTGTGGAGACAGATCCACATCAGTT 562
QY 62 GCCGGGCAAGTCAGAGATTAACACTATTAAATGGTATCAGCATAAACAGGGAAG 121
DB 563 GCCGGGCAAGTCAGAGATTAACACTATTAAATGGTATCAGCATAAACAGGGAAG 622
QY 122 CCCCTAAGCTCTGATCTATGTCATCCAGTTTGCAGAGTGGGGTCCCATCAAGTTCA 181
DB 623 CCCCTAAGCTCTGATCTATGTCATCCAGTTTGCAGAGTGGGGTCCCATCAAGTTCA 682
QY 182 GTGCAGTGGATATGGACAGATTCCTCTCAACATCAGCAGTCTGCAGCTGAAGATT 241
DB 683 GTGCAGTGGATCTGGACAGATTCCTCTCAACATCAGCAGTCTGCAGCTGAAGATT 742
QY 242 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCTGTAACATTTTGGCCAGGGGACCA 301
DB 743 TTGCAACTTACTACTGTCAAGAGAGTCTCAGTGCCTCTGTAACATTTTGGCCAGGGGACCA 802
QY 302 AGGTGGAGATCAACG 317
DB 803 AGGTGGAGATCAACG 818

RESULT 14
US-09-848-798-201
; Sequence 201, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.

; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 201
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH16
US-09-848-798-201

Query Match 86.9%; Score 276.4; DB 10; Length 321;
Best Local Similarity 91.8%; Pred. No. 5.1e-83;
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 1 GAGTCACTCAGTCTCCATCCCTGCTGCACTCTGTGGAGACAGATCCACATCAGT 60
DB 4 GAGTCACTCAGTCTCCATCCCTGCTGCACTCTGTGGAGACAGATCCACATCAGT 63
QY 61 TGCCGGCAAGTCAGAGATTAACACTATTAAATGGTATCAGCATAAACAGGGA 120
DB 64 TGCCGGCAAGTCAGAGATTAACACTATTAAATGGTATCAGCATAAACAGGGA 123
QY 121 GCCCTAAGCTCTGATCTATGTCATCCAGTTTGCAGAGTGGGGTCCCATCAAGTTT 180
DB 124 GCCCTAAGCTCTGATCTATGTCATCCAGTTTGCAGAGTGGGGTCCCATCAAGTTT 183
QY 181 AGTGCAGTGGATATGGACAGATTCCTCTCAACATCAGCAGTCTGCAGCTGAAGATT 240
DB 184 AGTGCAGTGGATATGGACAGATTCCTCTCAACATCAGCAGTCTGCAGCTGAAGATT 243
QY 241 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCTGTAACATTTTGGCCAGGGGACC 300
DB 244 TTGCAACTTACTACTGTCAAGAGATTCAGATCCCTCCCACTTCGGCGGAGGACC 303
QY 301 AAGGTGGAGATCAACGA 318
DB 304 AAGGTGGAGATCAACGA 321

RESULT 15
US-09-848-798-211
; Sequence 211, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 211
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH36
US-09-848-798-211

Query Match 86.9%; Score 276.4; DB 10; Length 321;
Best Local Similarity 91.8%; Pred. No. 5.1e-83;
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy	1	GAGTCACTCAGTCTCCATCCCTGCTGCTGCACTCTGTGGAGACAGAGTCACCATCAGT	60
Db	4	GAGTCACTCAGTCTCCATCCCTGCTGCTGCACTCTGTGGAGACAGAGTCACCATCACT	63
Qy	61	TGCCGGCAAGTCAGAGATTAAACACCTATTATATTTGGTATCAGCATAAACCCAGGAAA	120
Db	64	TGCCGGCAAGTCAGAGATTAGACGCTATTATAATTTGGTATCAGCAAAACCCAGGAAA	123
Qy	121	GCCCTAAGCTCCTGATCTATGCTGCACTCCAGTTTGCAAGTGGGTCCCATCAAGGTTT	180
Db	124	TCCCTAAGCTCCTGATCTATGCTGCACTCCAGTTTGCAAGTGGGTCCCATCAAGGTTT	183
Qy	181	AGTGGCAGTGGATATGGACACAGCTTCACTCTACCATCAGCAGTCTGCAACCTGAAGAT	240
Db	184	AGTGGCAGTGGATCTGGACACAGATTTCATCTACCATCAGCAGTCTGCAACCTGAAGAT	243
Qy	241	TTTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGCTACACTTTTGGCCAGGGACC	300
Db	244	TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCCGGCTTTGGGCCCTGGGACC	303
Qy	301	AAGTGGAGATCAAAACGA	318
Db	304	AAAGTGGATATCAAAACGA	321

Search completed: August 13, 2004, 19:18:23
Job time : 707.827 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 00:21:37 ; Search time 44.9697 Seconds
(without alignments)
3924.296 Million cell updates/sec

Title: US-10-027-725A-4

Perfect score: 318

Sequence: 1 gagctcactcagctccatc.....ccagggtgagatcaaacga 318

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	281.2	88.4	321	3	US-09-240-274-102
3	281.2	88.4	321	3	US-09-240-274-109
4	281.2	88.4	321	3	US-09-240-274-218
5	279.6	87.9	321	3	US-09-240-274-107
6	279.6	87.9	321	3	US-09-240-274-113
7	279.6	87.9	321	3	US-09-240-274-221
8	279.6	87.9	321	3	US-09-240-274-222
9	276.4	86.9	321	3	US-09-240-274-201
10	276.4	86.9	321	3	US-09-240-274-211
11	276.2	86.9	324	3	US-09-240-274-101
12	276.2	86.9	324	3	US-09-240-274-112
13	276.2	86.9	324	3	US-09-240-274-210
14	274.8	86.4	321	3	US-09-240-274-105
15	274.8	86.4	321	3	US-09-240-274-216
16	273.2	85.9	321	3	US-09-240-274-104
17	273.2	85.9	321	3	US-09-240-274-106
18	273.2	85.9	321	3	US-09-240-274-215
19	273.2	85.9	321	3	US-09-240-274-217
20	273	85.8	324	3	US-09-240-274-206
21	271.4	85.3	714	4	US-09-240-274-110
22	270.6	85.1	714	4	US-09-472-087-62
23	270	84.9	321	3	US-09-240-274-205
24	270	84.9	321	3	US-09-240-274-207
25	268.2	84.3	324	3	US-09-240-274-224
26	266.8	83.9	321	3	US-09-240-274-108
27	266.8	83.9	321	3	US-09-240-274-203

Sequence 103, App
Sequence 47, Appl
Sequence 48, Appl
Sequence 13, Appl
Sequence 200, App
Sequence 213, App
Sequence 23, Appl
Sequence 44, Appl
Sequence 50, Appl
Sequence 358, App
Sequence 206, App
Sequence 212, App
Sequence 49, Appl
Sequence 208, App
Sequence 114, App
Sequence 198, App
Sequence 31, Appl
Sequence 33, Appl

ALIGNMENTS

RESULT 1

US-09-240-274-199
; Sequence 199, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 199
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-240-274-199

Query Match	90.4%	Score 287.6;	DB 3;	Length 321;
Best Local Similarity	94.0%	Pred. No. 4e-91;		
Matches 299;	Conservative 0;	Mismatches 19;	Indels 0;	Gaps 0;
Qy	1	GAGTCACTCAGTCTCCATCCTCCCTGTCTGCACTCTGTGGGAGACAGAGTCACCATCAGT	60	
Db	4	GAGTCACTCAGTCTCCATCCTCCCTGTCTGCACTCTGTGGGAGACAGAGTCACCATCAGT	63	
Qy	61	TGCGGGCAGTCAGAGATTAACCTATTTAAATGGTATCAGCATTAACAGGAAA	120	
Db	64	TGCGGGCAGTCAGAGATTAACCTATTTAAATGGTATCAGCATTAACAGGAAA	123	
Qy	121	GCCCTAAGCTCTGTATCTATGTCATCCAGTTTGCAAGTGGGTCCCATCAAGTTTC	180	
Db	124	GCCCTAAGCTCTGTATCTATGTCATCCAGTTTGCAAGTGGGTCCCATCAAGTTTC	183	
Qy	181	AGTGGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGACCTTGAAGAT	240	
Db	184	AGTGGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGACCTTGAAGAT	243	
Qy	241	TTTGCAGTTACTACTGTCAAGAGAGTCTCAGTCCCTGCTACACTTTTGGCCAGGGACC	300	
Db	244	TTTGCAGTTACTACTGTCAAGAGAGTCTCAGTCCCTGCTACACTTTTGGCCAGGGACC	303	
Qy	301	AAGTGGAGATCAACGA	318	

Db 64 TCGCGGCAAGTCAGAGCATTTAGCAGCTATTTAAATTTGGTATCAGCAAAACACAGGAA 123
Qy 121 GCCCTTAAGCTCCCTGATCTATGCTGCATCCAGTTTGAAAGTGGGTCCTCCATCAAGGTTT 180
Db 124 GCCCTTAAGCTCCCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGTCCTCCATCAAGGTTT 183
Qy 181 AGTGGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCCTGAAGAT 240
Db 184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCACACCTGAAGAT 243
Qy 241 TTTCAGATTACTACTGTCAAGAGAGTCTCAGTCCCTGCTACACTTTTGGCCAGGGGACC 300
Db 244 TTTCAGATTACTACTGTCAACAGAGTTACAGTACCCTGGACGTTTCGGCCAGGGGACC 303
Qy 301 AAGGTGGAGATCAACGA 318
Db 304 AAGGTGGAAATCAACGA 321

RESULT 5

US-09-240-274-107
; Sequence 107, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 107
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I07
US-09-240-274-107

Query Match 87.9%; Score 279.6; DB 3; Length 321;
Best Local Similarity 92.5%; Pred. No. 2.5e-88;
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
Qy 1 GAGCTCACTCAGTCTCCATCTCCTCTGTCATCTGTGGGACAGAGTCACCATCAGT 60
Db 4 GAGCTCACTCAGTCTCCATCTCCTCTGTCATCTGTAGGACAGAGTCACCATCAGT 63
Qy 61 TCGCGGCAAGTCAGAGCATTTAGCAGCTATTTAAATTTGGTATCAGCAAAACACAGGAA 120
Db 64 TCGCGGCAAGTCAGAGCATTTAGCAGCTATTTAAATTTGGTATCAGCAAAACACAGGAA 123
Qy 121 GCCCTTAAGCTCCCTGATCTATGCTGCATCCAGTTTGAAAGTGGGTCCTCCATCAAGGTTT 180
Db 124 GCCCTTAAGCTCCCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGTCCTCCATCAAGGTTT 183
Qy 181 AGTGGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCCTGAAGAT 240
Db 184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCACACCTGAAGAT 243
Qy 241 TTTCAGATTACTACTGTCAAGAGAGTCTCAGTCCCTCGTACACTTTTGGCCAGGGGACC 300
Db 244 TTTCAGATTACTACTGTCAACAGAGTTACAGTACCCTCGAACTTTTCGGCCAGGGGACC 303
Qy 301 AAGGTGGAGATCAACGA 318
Db 304 AAGGTGGAGATCAACGA 321

RESULT 6

US-09-240-274-113
; Sequence 113, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 113
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I13
US-09-240-274-113

Query Match 87.9%; Score 279.6; DB 3; Length 321;
Best Local Similarity 92.5%; Pred. No. 2.5e-88;
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
Qy 1 GAGCTCACTCAGTCTCCATCTCCTCTGTCATCTGTGGGACAGAGTCACCATCAGT 60
Db 4 GAGCTCACTCAGTCTCCATCTCCTCTGTCATCTGTAGGACAGAGTCACCATCAGT 63
Qy 61 TCGCGGCAAGTCAGAGCATTTAGCAGCTATTTAAATTTGGTATCAGCAAAACACAGGAA 120
Db 64 TCGCGGCAAGTCAGAGCATTTAGCAGCTATTTAAATTTGGTATCAGCAAAACACAGGAA 123
Qy 121 GCCCTTAAGCTCCCTGATCTATGCTGCATCCAGTTTGAAAGTGGGTCCTCCATCAAGGTTT 180
Db 124 GCCCTTAAGCTCCCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGTCCTCCATCAAGGTTT 183
Qy 181 AGTGGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCCTGAAGAT 240
Db 184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCACACCTGAAGAT 243
Qy 241 TTTCAGATTACTACTGTCAAGAGAGTCTCAGTCCCTCGTACACTTTTGGCCAGGGGACC 300
Db 244 TTTCAGATTACTACTGTCAACAGAGTTACAGTACCCTCGAACTTTTCGGCCAGGGGACC 303
Qy 301 AAGGTGGAGATCAACGA 318
Db 304 AAGGTGGAGATCAACGA 321

RESULT 7

US-09-240-274-221
; Sequence 221, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 221

LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH52
US-09-240-274-221

Query Match
Best Local Similarity 87.9%; Score 279.6; DB 3; Length 321;
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 GAGCTCACTCAGTCCATCCCTCCCTGCTGCTGATCTGTGGGAGACAGAGTCCACCATCACT 60
DB 4 GAGCTCACTCAGTCCATCCCTCCCTGCTGCTGATCTGTGGGAGACAGAGTCCACCATCACT 63

QY 61 TGCCGGGCAAGTCAGAGATTAACACCTATTAAATTTGGTATCAGCATAAACCCAGGAAA 120
DB 64 TGCCGGGCAAGTCAGAGATTAACACCTATTAAATTTGGTATCAGCATAAACCCAGGAAA 123

QY 121 GCCCTAAGCTCCTGATCTATGCTGATCCAGTCTTGGCAAGTGGGTCCTCAACAGGTTTC 180
DB 124 GCCCTAAGCTCCTGATCTATGCTGATCCAGTCTTGGCAAGTGGGTCCTCAACAGGTTTC 183

QY 181 AGTGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCTCAAGAT 240
DB 184 AGTGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCTCAAGAT 243

QY 241 TTTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGCTACACTTTTGGCCAGGGACC 300
DB 244 TTTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGCTACACTTTTGGCCAGGGACC 303

QY 301 AAGGTGGAGATCAACGA 318
DB 304 AAGGTGGAATCAACGA 321

RESULT 8
US-09-240-274-222
Sequence 222, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 222
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-240-274-222

Query Match
Best Local Similarity 87.9%; Score 279.6; DB 3; Length 321;
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 GAGCTCACTCAGTCCATCCCTCCCTGCTGCTGATCTGTGGGAGACAGAGTCCACCATCACT 60
DB 4 GAGCTCACTCAGTCCATCCCTCCCTGCTGCTGATCTGTGGGAGACAGAGTCCACCATCACT 63

QY 61 TGCCGGGCAAGTCAGAGATTAACACCTATTAAATTTGGTATCAGCATAAACCCAGGAAA 120
DB 64 TGCCGGGCAAGTCAGAGATTAACACCTATTAAATTTGGTATCAGCATAAACCCAGGAAA 123

QY 121 GCCCTAAGCTCCTGATCTATGCTGATCCAGTCTTGGCAAGTGGGTCCTCAACAGGTTTC 180
DB 124 GCCCTAAGCTCCTGATCTATGCTGATCCAGTCTTGGCAAGTGGGTCCTCAACAGGTTTC 183

QY 181 AGTGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCTCAAGAT 240
DB 184 AGTGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCTCAAGAT 243

QY 241 TTTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGCTACACTTTTGGCCAGGGACC 300
DB 244 TTTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGCTACACTTTTGGCCAGGGACC 303

QY 301 AAGGTGGAGATCAACGA 318
DB 304 AAGGTGGAATCAACGA 321

RESULT 9
US-09-240-274-201
Sequence 201, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 201
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH16
US-09-240-274-201

Query Match
Best Local Similarity 86.9%; Score 276.4; DB 3; Length 321;
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 GAGCTCACTCAGTCCATCCCTCCCTGCTGCTGATCTGTGGGAGACAGAGTCCACCATCACT 60
DB 4 GAGCTCACTCAGTCCATCCCTCCCTGCTGCTGATCTGTGGGAGACAGAGTCCACCATCACT 63

QY 61 TGCCGGGCAAGTCAGAGATTAACACCTATTAAATTTGGTATCAGCATAAACCCAGGAAA 120
DB 64 TGCCGGGCAAGTCAGAGATTAACACCTATTAAATTTGGTATCAGCATAAACCCAGGAAA 123

QY 121 GCCCTAAGCTCCTGATCTATGCTGATCCAGTCTTGGCAAGTGGGTCCTCAACAGGTTTC 180
DB 124 GCCCTAAGCTCCTGATCTATGCTGATCCAGTCTTGGCAAGTGGGTCCTCAACAGGTTTC 183

QY 181 AGTGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCTCAAGAT 240
DB 184 AGTGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCTCAAGAT 243

QY 241 TTTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGCTACACTTTTGGCCAGGGACC 300
DB 244 TTTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGCTACACTTTTGGCCAGGGACC 303

QY 301 AAGGTGGAGATCAACGA 318
DB 304 AAGGTGGAATCAACGA 321

RESULT 10
US-09-240-274-211


```
; Sequence 211, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 211
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH36
US-09-240-274-211

Query Match      86.9%; Score 276.4; DB 3; Length 321;
Best Local Similarity 91.8%; Pred. No. 3.4e-87;
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 GAGTCACTCAGTCTCCATCTCCTGTCTGTCATCTGTGGGAGACAGAGTCACCATCAGT 60
Db 4 GAGTCACTCAGTCTCCATCTCCTGTCTGTCATCTGTGGGAGACAGAGTCACCATCAGT 63
QY 61 TCCGGGCAAGTCAGAGCAATTAACACCTATTAAATTGGTATCAGCATTAACACAGGAAA 120
Db 64 TCCGGGCAAGTCAGAGCAATTAACACCTATTAAATTGGTATCAGCATTAACACAGGAAA 123
QY 121 GCCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAGTGGGTGCCATCAAGGTTTC 180
Db 124 TCCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAGTGGGTGCCATCAAGGTTTC 183
QY 181 AGTGGAGTGATATGGACAGACTTCACTCTCACCATCAGAGCTCTGCAGCCTGAAGAT 240
Db 184 AGTGGAGTGATATGGACAGACTTCACTCTCACCATCAGAGCTCTGCAGCCTGAAGAT 243
QY 241 TTGCAAGTTACTACTCTCAAGAGAGTCTCAGTGCC--TCGTACACTTTTGGCCAGGACC 297
Db 244 TTGCAAGTTACTACTCTCAAGAGAGTCTCAGTGCC--TCGTACACTTTTGGCCAGGACC 300
QY 301 AAGTGGAGATCAACGA 318
Db 304 AAGTGGAGATCAACGA 321

RESULT 11
US-09-240-274-101
; Sequence 101, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 324
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I12
US-09-240-274-112
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; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I01
US-09-240-274-101

Query Match      86.9%; Score 276.2; DB 3; Length 324;
Best Local Similarity 93.5%; Pred. No. 4e-87;
Matches 300; Conservative 0; Mismatches 18; Indels 3; Gaps 1;

QY 1 GAGTCACTCAGTCTCCATCTCCTGTCTGTCATCTGTGGGAGACAGAGTCACCATCAGT 60
Db 4 GAGTCACTCAGTCTCCATCTCCTGTCTGTCATCTGTGGGAGACAGAGTCACCATCAGT 63
QY 61 TCCGGGCAAGTCAGAGCAATTAACACCTATTAAATTGGTATCAGCATTAACACAGGAAA 120
Db 64 TCCGGGCAAGTCAGAGCAATTAACACCTATTAAATTGGTATCAGCATTAACACAGGAAA 123
QY 121 GCCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAGTGGGTGCCATCAAGGTTTC 180
Db 124 GCCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAGTGGGTGCCATCAAGGTTTC 183
QY 181 AGTGGAGTGATATGGACAGACTTCACTCTCACCATCAGAGCTCTGCAGCCTGAAGAT 240
Db 184 AGTGGAGTGATATGGACAGACTTCACTCTCACCATCAGAGCTCTGCAGCCTGAAGAT 243
QY 241 TTGCAAGTTACTACTCTCAAGAGAGTCTCAGTGCC--TCGTACACTTTTGGCCAGGACC 297
Db 244 TTGCAAGTTACTACTCTCAAGAGAGTCTCAGTGCC--TCGTACACTTTTGGCCAGGACC 303
QY 298 ACCAAGTGGAGATCAACGA 318
Db 304 ACCAAGTGGAGATCAACGA 324

RESULT 12
US-09-240-274-112
; Sequence 112, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 112
; LENGTH: 324
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I12
US-09-240-274-112

Query Match      86.9%; Score 276.2; DB 3; Length 324;
Best Local Similarity 93.5%; Pred. No. 4e-87;
Matches 300; Conservative 0; Mismatches 18; Indels 3; Gaps 1;

QY 1 GAGTCACTCAGTCTCCATCTCCTGTCTGTCATCTGTGGGAGACAGAGTCACCATCAGT 60
Db 4 GAGTCACTCAGTCTCCATCTCCTGTCTGTCATCTGTGGGAGACAGAGTCACCATCAGT 63
QY 61 TCCGGGCAAGTCAGAGCAATTAACACCTATTAAATTGGTATCAGCATTAACACAGGAAA 120
Db 64 TCCGGGCAAGTCAGAGCAATTAACACCTATTAAATTGGTATCAGCATTAACACAGGAAA 123
QY 121 GCCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAGTGGGTGCCATCAAGGTTTC 180
Db 124 GCCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAGTGGGTGCCATCAAGGTTTC 183
```

Qy	181	AGTGGCAGTGGATATGGGACACAGACTTCACTCTCACCATCAGCAGTCTCGAGCCTGAAGAT	240
Db	184	AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT	243
Qy	241	TTTTCGAGTTTACTACTGTTCAGAGAGAGTCTCAGTGCCTCTGACACCTTTTGGCCAGGGG	297
Db	244	TTTTCGACCTTACTACTGTTCACAGAGATTACAGTACCCCTCCGTCACACTTTTGGCCAGGGG	303
Qy	298	ACCAAGGTGGAGATCAACAGA	318
Db	304	ACCAAGCTGGAGATCAACAGA	324

```

; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I05
US-09-240-274-105

```

Query Match 86.4%; Score 274.8; DB 3; Length 321;
Best Local Similarity 91.5%; Pred. No. 1.2e-86;
Matches 291; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY	1	GAGCTCACTCAGTCTCCATCTCCCTGCTGTGCACTCTGTGGGAGACAGAGTCACCATCAGT	60
Db	4	GAGTCACCCAGTCTCCATCTCCCTGCTGTGCACTCTGTAGGAGACAGAGTCACCATCACT	63
QY	61	TGCGGGCAAGTCAGAGAATTAACCTATTTAAATTGGTATCAGCATAAACCAGGGAAA	120
Db	64	TGCGGGCAAGTCAGAGCAATTAGCACTATTTAAATTGGTATCAGCAGAAACCAGGAAAA	123
QY	121	GCCCTTAAGTCTCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGTCCCATCAAGTTC	180
Db	124	GCCCTTAACCTCTCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGTCCCATCAAGTTC	183
QY	181	AGTGGCAGTGGATATGGGACAGACTTCACCTCTACCATCAGCAGTCTGCAGCCTGAAGAT	240
Db	184	AGTGGCAGTGGATCTGGGACAGATTTCACTCTACCATCAGCAGTCTGCACCTGAAGAT	243
QY	241	TTTGCAAGTTACTACTGCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGGACC	300
Db	244	TTTGCAACTTACTACTGCAACAGAGTTACAGTTATCTCGCACGTTTCGGCCAAAGGGACC	303
QY	301	AGGTGGAGATCAACGA	318
Db	304	AGGTGGAGATCAGACGA	321

Search completed: August 13, 2004, 07:18:09
Job time : 45.9697 secs

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OM nucleic - nucleic search, using sw model

Run on: August 12, 2004, 19:27:23 ; Search time 1368.2 Seconds
(without alignments)
10073.859 Million cell updates/sec

Title: US-10-027-725A-5

Perfect score: 318

Sequence: 1 gagctaccacgtctccatc.....ccaaactggagatcaaacga 318

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hrg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_ov.*

22: em_ph.*

23: em_pl.*

24: em_ro.*

25: em_sts.*

26: em_un.*

27: em_vi.*

28: em_hrg.*

29: em_hum.*

30: em_hrg_inv.*

31: em_hrg_inv.*

32: em_hrg_inv.*

33: em_hrg_inv.*

34: em_hrg_inv.*

35: em_hrg_inv.*

36: em_hrg_inv.*

37: em_hrg_inv.*

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39: em_hrg_inv.*

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45: em_hrg_inv.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	316.4	99.5	318	9	HSA458380	AJ458380 Homo sapi
2	281.2	88.4	321	9	HSIGVK110	X73860 H.sapiens m
3	278	87.4	322	9	HUMIGHGD	L03142 Homo sapien
4	278	87.4	326	9	HUMIGHGY	L03160 Homo sapien
5	277	87.1	830	9	AB064095	AB064095 Homo sapi
6	276.4	86.9	321	6	AR160973	AR160973 Sequence
7	276.4	86.9	321	6	AR161027	AR161027 Sequence
8	276.4	86.9	328	9	HUMIGHHC	L03164 Homo sapien
9	273.8	86.1	324	9	AB063929	AB063929 Homo sapi
10	273.8	86.1	324	9	AF107245	AF107245 Homo sapi
11	273.8	86.1	390	9	HSU43773	U43773 Human immu
12	273.8	86.1	828	9	AB064098	AB064098 Homo sapi
13	273.4	86.0	315	6	A68535	A68535 Sequence 51
14	273.4	86.0	315	9	HSLD220VL	Y08251 H.sapiens m
15	273.4	86.0	318	12	AF044451	AF044451 Synthetic
16	273.2	85.9	321	6	AR160978	AR160978 Sequence
17	273.2	85.9	321	6	AR160984	AR160984 Sequence
18	273.2	85.9	321	6	AR161029	AR161029 Sequence
19	273.2	85.9	321	6	AR161039	AR161039 Sequence
20	273.2	85.9	321	6	AR161046	AR161046 Sequence
21	273.2	85.9	321	9	HSIGVK16F	X73855 H.sapiens m
22	273.2	85.9	796	9	AB064138	AB064138 Homo sapi
23	272.6	85.7	311	9	HSX98989	X98989 H.sapiens r
24	272.2	85.6	387	12	AF453148	AF453148 Synthetic
25	272.2	85.6	429	9	HUMIGKW	M74019 Homo sapien
26	271.8	85.5	367	12	AF453190	AF453190 Synthetic
27	271.6	85.4	321	6	AR160977	AR160977 Sequence
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29	271.6	85.4	321	6	AR161049	AR161049 Sequence
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43	270.2	85.0	318	12	AF044462	AF044462 Synthetic
44	270	84.9	321	6	AR161043	AR161043 Sequence
45	270	84.9	321	6	AR161045	AR161045 Sequence

ALIGNMENTS

RESULT 1
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LOCUS HSA458380 318 bp mRNA linear PRI 30-APR-2002
DEFINITION Homo sapiens partial mRNA for immunoglobulin kappa light chain
variable region (IGKV gene), clone 60.
ACCESSION AJ458380
VERSION AJ458380.1 GI:20387059
KEYWORDS IGKV gene; immunoglobulin kappa; light chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Flicker,S., Steinberger,P., Norderhaug,L., Sperr,W.R., Majlesi,Y.,
Valent,P., Kraft,D. and Valenta,R.

Pred. No. is the number of results predicted by chance to have a

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TITLE
Conversion of grass allergen-specific human IgE into a protective
IgG1 antibody
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 318)
AUTHORS
Flicker S.
TITLE
Direct Submission
JOURNAL
Submitted (24-APR-2002) Flicker S., Department of Pathophysiology,
General Hospital of Vienna, 3Q, Waehringer Guertel 18-20, A-1090
Vienna, AUSTRIA
FEATURES
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region"
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Best Local Similarity	99.7%;	Pred. No. 9.5e-91;	
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Db	1	GAGCTCACCAGTCTCCATCTCTCCCTGTGTCCTCTGTAGGACACAGAGTCACCATCACT	60
QY	61	TGCCGGGCAGTCAGAGTTATTAGCACCTATTTAAATTGGTATCAGCAGAAAACCGGGGAAG	120
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QY	241	TTTTGCAAGTTACTACTGTCAACAGAGTTACCTTATATACCTTCGGCCCTGGGACC	300
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Db	301	AAACTGGAGATCAAACA	318

RESULT 2
 LOCUS HSIGVK110
 DEFINITION H.sapiens mRNA for Ig kappa light chain variable region
 (V-J), subgroup I (clone 10I).
 ACCESSION X73860
 VERSION X73860.1 GI:516249
 KEYWORDS autoantibody; Ig J-segment; Ig kappa light chain; Ig subgroup I; Ig variable region; immunoglobulin.
 SOURCE Homo sapiens (human)

ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Hexham, J.M., Furmaniak, J., Pegg, C., Burton, D.R. and Smith, B.R.
TITLE	Cloning of a human autoimmune response: preparation and sequencing of a human anti-thyroglobulin autoantibody using a combinatorial approach
JOURNAL	Autoimmunity 12 (2), 135-141 (1992)
MEDLINE	92314301
PUBMED	1617110
REFERENCE	2 (bases 1 to 321)
AUTHORS	Hexham, J.M., Partridge, L.J., Furmaniak, J., Petersen, V.B., Colls, J.C., Pegg, C., Rees-Smith, B. and Burton, D.R.
TITLE	Cloning and characterisation of TPO autoantibodies using combinatorial phage display libraries
JOURNAL	Autoimmunity 17 (3), 167-179 (1994)
MEDLINE	95035699
PUBMED	7524700
REFERENCE	3 (bases 1 to 321)
AUTHORS	Hexham, J.M., Partridge, L.J., Furmaniak, J., Petersen, V.B., Colls, J.C., Pegg, C.A.S., Rees-Smith, B. and Burton, D.R.
TITLE	Probing the human anti-thyroid peroxidase repertoire of a Hashimoto's thyroiditis patient using combinatorial phage display libraries
JOURNAL	Unpublished
REFERENCE	4 (bases 1 to 321)
AUTHORS	Hexham, J.
TITLE	Direct Submission
JOURNAL	Submitted (25-JUN-1993) J. Hexham, Univ. of Sheffield, Dept. of Mol. Biology and Biotechnology, P. O. Box 594, Firth Court, Western Bank, Sheffield S10 2PU, UK

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ORIGIN		/note="IgG1/K anti-thyroid peroxidase autoantibody Fab"
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Best Local Similarity		92.8%; Pred. No. 2.2e-79;
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Db      241  TTTCGAAGTTACTACTGTCACAGAGTTACACTTATATACCTTTCGGCCTGGGACC 300
QY      301  AAACCTGGAGATCAAAACGA 318
Db      301  AGCTGGAGATCAACGA 318

RESULT 5
AB064095      830 bp mRNA linear PRI 02-JUL-2002
LOCUS      Homo sapiens IGK mRNA for immunoglobulin kappa light chain VLJ
DEFINITION      region, partial cds, clone:K54.
ACCESSION      AB064095
VERSION        AB064095.1 GI:21669396
KEYWORDS
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE          Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
                Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
                Miura,K. and Kurosawa,Y.
                Construction and characterization of antibody libraries: isolation
                of therapeutic human antibodies and application to functional
                genomics
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 830)
AUTHORS      Kurosawa,Y.
TITLE        Direct Submission
JOURNAL      Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
                Comprehensive Medical Science, Fujita Health University;
                Kutsukake-cho, Toyooka 470-1192, Japan
                (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
                Please visit our web site
                URL:http://www.fujita-hu.ac.jp/immunity/.
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Matches 292; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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QY      302  AACTGGAGATCAAAACGA 318
Db      374  AGTGGATATCAACGA 390

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AR160973      321 bp DNA linear PAT 17-OCT-2001
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DEFINITION      AR160973
ACCESSION      AR160973
VERSION        AR160973.1 GI:16226189
KEYWORDS
SOURCE        Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 321)
AUTHORS        Siegel,D.L.
TITLE          Rh(D)-binding proteins and magnetically activated cell sorting
                method for production thereof
                Patent: US 6255455-A 102 03-JUL-2001;
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QY      301  AAACCTGGAGATCAAAACGA 318
Db      304  AGTGGAAATCAACGA 321

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JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 324)
 AUTHORS Kurosawa, Y.
 TITLE Direct Submission
 JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University; Kutsukake-cho, Toyooka 470-1192, Japan
 (E-mail: kurosawa@fujita-hu.ac.jp, Tel: 81-562-93-9387)
 COMMENT Please visit our web site
 URL: http://www.fujita-hu.ac.jp/immunity/
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ORIGIN

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 Matches 290; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

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 QY 122 CCCCTAAGCTCTGATCTGTAGTGCATCCAAATTTGCAAAAGTGGGTCCCATCCAGGTTCA 181
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 QY 242 TTGCAAGTTACTACTGTCAACAGAGTTACACTTATATACCTTTCGCCCTGGGACCA 301
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 QY 302 AACTGGAGATCAAAACGA 318
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 Db 308 AGCTGGAGATCAACGA 324

RESULT 10
 AF107245
 LOCUS AF107245 324 bp mRNA linear PRI 01-DEC-1999
 DEFINITION Homo sapiens clone MD05 immunoglobulin kappa light chain variable region mRNA, partial cds.
 ACCESSION AF107245
 VERSION AF107245.1 GI:6492200
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

1 (bases 1 to 324)
 Perera, W.S., Moss, M.T. and Urbaniak, S.J.
 Molecular Characterization Of Anti-RhD Antibodies: Antibody Repertoire, Affinity Maturation And Epitope Specificities Unpublished
 2 (bases 1 to 324)
 Perera, W.S., Moss, M.T., Urbaniak, S.J. and Fraser, R.
 Direct Submission
 Submitted (18-NOV-1998) Academic Transfusion Medicine Unit, Regional Transfusion Centre, Foresterhill Road, Foresterhill, Aberdeen, Scotland AB25 2ZW, UK

FEATURES
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CDS

Query Match 86.1%; Score 273.8; DB 9; Length 324;
 Best Local Similarity 91.5%; Pred. No. 5,3e-77;
 Matches 290; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

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ORIGIN

Query Match 86.1%; Score 273.8; DB 9; Length 324;
 Best Local Similarity 91.5%; Pred. No. 5,3e-77;
 Matches 290; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

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 Db 8 AGATGACCCAGTCTCCATCTCCCTGCTGTGATCTGTAGGAGACAGTCCACATCACTT 67
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 QY 302 AACTGGAGATCAAAACGA 318
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 Db 308 AGCTGGAGATCAACGA 324

RESULT 11
 HSU43773

LOCUS HSU43773 390 bp mRNA linear PRI 05-JUN-1996
 DEFINITION Human immunoglobulin light chain variable region mRNA, cell line 13d2, anti-RhD, partial cds.
 ACCESSION U43773
 VERSION U43773.1 GI:1353831
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 390)

AUTHORS	Boucher, G., Broly, H. and Lemieux, R.
TITLE	Restricted Use of Cationic Germline VH Gene Segments in Human Rh(b)
JOURNAL	Red Cell Antibodies
REFERENCE	Unpublished
AUTHORS	2 (bases 1 to 390)
TITLE	Boucher, G.
JOURNAL	Direct Submission
FEATURES	Submitted (21-DEC-1995) Gerard Boucher, Research and Development, The Canadian Red Cross Society, Transfusion Center of Quebec, 2535 Laurier Boulevard, Ste-Foy, Quebec G1V 4M3, Canada
source	Location/Qualifiers 1. .390

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136. .168
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Best Local Similarity	91.5%;	Pred. No.	5.3e-17;				
Matches	290;	Conservative	0;	Mismatches	27;	Indels	0;
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QY	2	AGCTCACCCAGTCTCCATCTCCTCGTCTCTCGCTCTGTAGGAGACAGAGTCACCATCACTT	61
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QY	62	GCCGGGCACTGCAGAGTATTAGCACCTATTATTAATTGGTATCAGCAGAAACCGGGGAAG	121
DB			
QY	134	GCCGGGCAAGTCAGAGCAITTAGCAGTATTATTAATTGGTATCAGCAGAAACCGAGGAAAG	193
DB			
QY	122	CCCTAAGCTCCTTGATCTGTAGTGCATCCAAATTTGCAAAAGTGGGGTCCCATCCAGGTTC	181
DB			
QY	194	CCCTTAGGCTCTGATCTATGCTGCAATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTC	253
DB			
QY	182	GTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCATCAGCAATCTGCACCTTGAAGACT	241
DB			
QY	254	GTGGCAGTGGATCTGGGACAGATTTCACCTCAACCATCAGCAGTCTGCACCTGAAGATT	313
DB			
QY	242	TTGCAAGTTACTACTGTCAACAGAGTTTACACTACCTTATATACCTTCGGCCCTGGGACCA	301
DB			
QY	314	TTGCAGTTACTACTGTCAACAGAGTTTCAATACCCCTATTCACTTTTCGGCCCTGGGACCA	373
DB			
QY	302	AACCTGGAGATCAAAACGA	318
DB			

Db	374	AAGTGATATCAACGA	390	
RESULT 12				
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LOCUS	AB064098	828 bp	mRNA	linear
DEFINITION	Homo sapiens IGH mRNA for immunoglobulin kappa light chain VLJ region, partial cds, clone:K57.			
ACCESSION	AB064098			
VERSION	AB064098.1	GI:21669402		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	1. Akahori Y., Iba Y., Morino K., Shinozaki M., Hirano Y., Kakita M., Suzuki K., Torii H., Ukai Y., Honda T., Katsumi H., Okada J., Mura K. and Kurosawa Y.			
TITLE	Construction and characterization of antibody libraries: isolation of the therapeutic human antibodies and application to functional genomics			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 828)			
AUTHORS	Kurosawa Y.			
TITLE	Direct Submission			
JOURNAL	Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University; Kutsukake-cho, Toyooka 470-1192, Japan			
COMMENT	(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387) Please visit our web site URL: http://www.fujita-hu.ac.jp/immunity/ .			
FEATURES	Location/Qualifiers			
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sig_peptide

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ORIGIN		/note="peirb signal peptide"				
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Matches 290;	Conservative 0;	Mismatches 27;	Indels 0;	Gaps 0;		
Qy	2	AGCTACCCAGTCTCCATCCTCTCCCTGTCCTCTGTAGGACACAGAGTCACCATCATT	61			
Db	74	AGATGACCCAGTCTCCATCCTCTCCCTGTCGTCGTAGGACACAGAGTCACCATCATT	133			
Qy	62	GCGGGCAGCTCAGAGTATTAGCACTATTTAAATTGGTATCAGCAGAAACCGGGGAGG	121			
Db	134	GCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCGGGGAAAG	193			
Qy	122	CCCTAAGCTCCTGATCTGTAGTGCATCCAAATTTCGAAAGTGGGGTCCCATCCAGGTTC	181			

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Db      194  CCCCTAAGCTCTGATCTATGCTGATCCAGTTTGCAAGTGGGTCCCATCAAGTTCA 253
QY      182  GTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGACT 241
Db      254  GTGGCAGTGGATCTGGGACAGAGTTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATT 313
QY      242  TTGCAAGTACTACTGTCAACAGAGTTACACTTACCTTATATACCTTCGGCCCTGGGACCA 301
Db      314  TTGCAACTTACTACTGTCAACAGAGTTACAGTACCCTGACCTTTTGGCCAGGGGACCA 373
QY      302  AACTGGAGATCAACCA 318
Db      374  AGCTGGAGATCAACGA 390

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RESULT 13
LOCUS   A68535                      315 bp      DNA      linear      PAT 06-MAY-1999
DEFINITION
Sequence 51 from Patent WO9749809.
ACCESSION
A68535
VERSION
A68535.1 GI:4759587
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
Miescher, S., Vogel, M., Stadler, B., Morell, A., Imboden, M. and
Amstutz, H.
TITLE
POLYPEPTIDES CAPABLE OF FORMING ANTIGEN BINDING STRUCTURES WITH
SPECIFICITY FOR THE RHESUS D ANTIGENS, THE DNA ENCODING THEM AND
THE PROCESS FOR THEIR PREPARATION AND USE
JOURNAL
Patent: WO 9749809-A 51 31-DEC-1997;
ROTKREUZSTIFTUNG ZENTRALLAB (CH)
FEATURES
Location/Qualifiers
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DIK"

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CDS
Query Match      86.0%; Score 273.4; DB 6; Length 315;
Best Local Similarity 91.7%; Pred. No. 7.2e-77;
Matches 289; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY      1  GAGTCACCCAGTCTCCATCCCTCCCTGCTGCTAGGACAGAGTCCACATCACT 60
Db      1  GTGATACCCAGTCTCCATCCCTCCCTGCTGCTAGGACAGAGTCCACATCACT 60
QY      61  TGC CGGGCAGCTCAGAGTATTAGCAGCTATTAAATTGGTATCAGAGAAACCGGGGAAG 120
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QY      121  GCCCTTAAGTCTCTGATCTCTAGTGCATCCAAATTGCAAGTGGGTCCCATCAAGTTTC 180

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ORIGIN

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Query Match      86.0%; Score 273.4; DB 6; Length 315;
Best Local Similarity 91.7%; Pred. No. 7.2e-77;
Matches 289; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY      1  GAGTCACCCAGTCTCCATCCCTCCCTGCTGCTAGGACAGAGTCCACATCACT 60
Db      1  GTGATACCCAGTCTCCATCCCTCCCTGCTGCTAGGACAGAGTCCACATCACT 60
QY      61  TGC CGGGCAGCTCAGAGTATTAGCAGCTATTAAATTGGTATCAGAGAAACCGGGGAAG 120
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Db      121  GCCCTTAAGTCTCTGATCTCTAGTGCATCCAGTTTTCAAAGTGGGTCCCATCAAGTTTC 180
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QY      241  TTTGCAAGTACTACTGTCAACAGAGTTACACTTATATACCTTCGGCCCTGGGACC 300
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QY      301  AAAGTGGATCAAA 315
Db      301  AAAGTGGATCAAA 315

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RESULT 14
LOCUS   HSLD220VL                  315 bp      mRNA      linear      PRI 07-OCT-1996
DEFINITION
H. sapiens mRNA for variable region of immunoglobulin kappa light
chain, clone LD2-20-VL.
ACCESSION
Y08251
VERSION
Y08251.1 GI:1561609
KEYWORDS
Ig kappa chain; immunoglobulin; light chain; variable region.
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
Miescher, S.M.
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 315)
AUTHORS
Miescher, S.M.
TITLE
Direct Submission
JOURNAL
Submitted (19-SEP-1996) S.M. Miescher, Institute of Immunology and
Allergy, University of Bern, Sahli Haus 2, Inselspital, CH-3010
Bern, SWITZERLAND
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Location/Qualifiers
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FEATURES

source

CDS

ORIGIN

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Query Match      86.0%; Score 273.4; DB 9; Length 315;
Best Local Similarity 91.7%; Pred. No. 7.2e-77;
Matches 289; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY      1  GAGTCACCCAGTCTCCATCCCTCCCTGCTGCTAGGACAGAGTCCACATCACT 60
Db      1  GTGATACCCAGTCTCCATCCCTCCCTGCTGCTAGGACAGAGTCCACATCACT 60
QY      61  TGC CGGGCAGCTCAGAGTATTAGCAGCTATTAAATTGGTATCAGAGAAACCGGGGAAG 120
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Qy 301 AAAGTGGAGATCAAA 315
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RESULT 15
LOCUS AF044451 318 bp mRNA linear SYN 31-OCT-2001
DEFINITION Synthetic construct from Homo sapiens clone 102 anti-Rh(D) antibody
v kappa segment mRNA, partial cds.
ACCESSION AF044451
VERSION AF044451.1 GI:3046473
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 318)
AUTHORS Siegel,D.L., Chang,T.Y., Russell,S.L. and Bunya,V.Y.
TITLE Isolation of cell surface-specific human monoclonal antibodies
using phage display and magnetically-activated cell sorting:
applications in immunohematology
J. Immunol. Methods 206 (1-2), 73-85 (1997)
JOURNAL 97469098
MEDLINE 9328570
PUBMED
REFERENCE 2 (bases 1 to 318)
AUTHORS Chang,T.Y. and Siegel,D.L.
TITLE Genetic and immunological properties of phage-displayed human
anti-Rh(D) antibodies: implications for Rh(D) epitope topology
Blood 91 (8), 3066-3078 (1998)
JOURNAL 98200617
MEDLINE 9531621
PUBMED
REFERENCE 3 (bases 1 to 318)
AUTHORS Chang,T.Y., Russell,S.L., Bunya,V.Y. and Siegel,D.L.
TITLE Direct Submission
Submitted (26-JAN-1998) Path & Lab Med, University of Pennsylvania,
36th & Hamilton, Philadelphia, PA 19104, USA
JOURNAL
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Matches 289; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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Db 4 GAGTCAACCCAGTCTCCATCCTTCCTCTGTGCTCTGTAGGAGACAGAGTCACCATCACT 63

Qy 61 TCCGGGCGAGTCTCAGAGTATTAGCACCTATTAAATTGGTATCAGCAGAAACCGGGGAAG 120
Db 64 TCCGGGCGAGTCTCAGAGTATTAGCAGCTATTAAATTGGTATCAGCAGAAACCGAGGAAA 123

Qy 121 GCCCTAAGCTCCTGATCTGTAGTGCATCCAAATTTGCAAAAGTGGGTCCCATCCAGGTC 180
Db 124 GCCCTAAGCTCCTGATCTGTAGTGCATCCAAATTTGCAAAAGTGGGTCCCATCAAGGTC 183

Qy 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCCATCAGCAATCTGCAACCTGAAGAC 240
Db 184 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCCATCAGCAATCTGCAACCTGAAGAT 243

Qy 241 TTTCAGAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
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Job time : 1369.2 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 00:12:28 ; Search time 1864.96 Seconds
(without alignments)
5091.898 Million cell updates/sec

Title: US-10-027-725A-5

Perfect score: 318

Sequence: 1 gagctcaccagcttcctatc.....ccaaactggagatcaaacga 318

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

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20: em_gss_vit:*

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22: em_gss_nam:*

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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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5	269	84.6	770	12	BG685444
6	269	84.6	797	14	CB987347
7	267.4	84.1	525	14	CD705928
8	267.4	84.1	750	14	CB985395
9	265.8	83.6	431	10	AW406886
10	265.8	83.6	693	14	CD684441
11	265.8	83.6	799	14	CB984750
12	265.8	83.6	819	14	CB985931
13	265.8	83.6	864	12	BG548281
14	265.8	83.6	933	13	BQ899146
15	265.8	83.6	992	13	BQ708832
16	264.2	83.1	391	10	AW404992
17	264.2	83.1	447	10	AW405752
18	264.2	83.1	487	10	AW405301
19	264.2	83.1	498	14	CD684450
20	264.2	83.1	499	14	CD685478
21	264.2	83.1	608	10	AW404714
22	264.2	83.1	619	14	CD693603
23	264.2	83.1	724	14	CB959008
24	264.2	83.1	745	14	CB958128
25	264.2	83.1	748	14	CB956867
26	262.8	82.6	471	10	AW406294
27	262.6	82.6	550	14	CD709957
28	262.6	82.6	708	14	CB956923
29	262.6	82.6	725	14	CB987519
30	262.6	82.6	742	14	CB984723
31	262.6	82.6	923	13	BQ882857
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33	261.2	82.1	1067	13	BX397739
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35	261	82.1	671	12	BM830977
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37	261	82.1	753	14	CB955708
38	261	82.1	855	14	CB995312
39	259.4	81.6	460	10	AW405906
40	259.4	81.6	532	12	BM823145
41	259.4	81.6	566	10	AW406081
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ALIGNMENTS

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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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IMAGE:3061128 5', mRNA sequence.
AW407904
AW407904.1 GI:6926961
EST.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 422)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/JLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

AW407904
UI-HF-BL0-add-a-01-0-UI.r2 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3061128 5', mRNA sequence.
AW407904
AW407904.1 GI:6926961
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 422)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/JLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: M13 Forward.

FEATURES source

Location/Qualifiers
 1. 493

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3057290"

/tissue type="lymph"

/cell type="germinal center B cells"

/cell_line="MGC85"

/lab_host="DH10B (LTI)"

/clone_lib="NIH MGC 37"

/note="Vector: p7T3-Pac; Site 1: NotI; Site 2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (1.5-2.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. Library preparation by Maria de Fatima
 Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 84.6%; Score 269; DB 10; Length 493;

Best Local Similarity 90.5%; Pred. No. 9, 7e-71;

Matches 287; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 2 AGCTACCCAGTCTCCATCCCTCCCTGCTGCTGTAGGACAGAGTCAACCATCACTT 61

Db 79 AGATGACCCAGTCTCCATCCCTCCCTGCTGCTGTAGGACAGAGTCAACCATCACTT 138

Qy 62 GCCGGGACGTCAGAGTATTAGCACTTATTAAATTGGTATCAGAGAAACCGGGAGG 121

Db 139 GCCGGGACGTCAGAGTATTAGCACTTATTAAATTGGTATCAGAGAAACCGGGAGG 198

Qy 122 CCCCTAAGCTCTGATCTGTAGTGCATCCCAATTTGCAAGTGGGTCCCATCCAGGTTC 181

Db 199 CCCCTAAGCTCTGATCTGTAGTGCATCCCAATTTGCAAGTGGGTCCCATCCAGGTTC 258

Qy 182 GTGCAGTGTATCTGGACAGAGTTCATCTCCATCAGCAATCTGCAACCTGAAGACT 241

Db 259 GTGCAGTGTATCTGGACAGAGTTCATCTCCATCAGCAATCTGCAACCTGAAGACT 318

Qy 242 TTGCAAGTTACTACTGTCACAGAGTTACACTATATACCTTCGGCCCTGGGACCA 301

Db 319 TTGCAAGTTACTACTGTCACAGAGTTACACTATATACCTTCGGCCCTGGGACCA 378

Qy 302 AACTGGAGATCAACGA 318

Db 379 AGGTGGAATCAACGA 395

RESULT 4

CD690145

LOCUS

DEFINITION EST6668 human nasopharynx Homo sapiens cDNA, mRNA sequence.

CD690145

VERSION CD690145.1 GI:32210615

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 624)

Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and

Zeng, Y.-X.

Transcriptional Gene Expression Profile of Human Nasopharynx

Unpublished (2003)

Contact: Yixin Zeng

Cancer Center

Sun Yat-sen University

651 DongFeng Road East, Guangzhou 510060, China
 Tel: 86-1380-9770-743
 Fax: 86-20-8775-4506
 Email: yxzeng@gzsums.edu.cn.

FEATURES

source

Location/Qualifiers

1. 624

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/tissue type="normal nasopharynx"

/clone_lib="human nasopharynx"

/note="ESTs generated from a normal nasopharynx cDNA

library from southern Chinese"

ORIGIN

Query Match 84.6%; Score 269; DB 14; Length 624;

Best Local Similarity 90.5%; Pred. No. 1.1e-70;

Matches 287; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 2 AGCTACCCAGTCTCCATCCCTCCCTGCTGCTGTAGGACAGAGTCAACCATCACTT 61

Db 121 AGATGACCCAGTCTCCATCCCTCCCTGCTGCTGTAGGACAGAGTCAACCATCACTT 180

Qy 62 GCCGGGACGTCAGAGTATTAGCACTTATTAAATTGGTATCAGAGAAACCGGGAGG 121

Db 181 GCCGGGACGTCAGAGTATTAGCACTTATTAAATTGGTATCAGAGAAACCGGGAGG 240

Qy 122 CCCCTAAGCTCTGATCTGTAGTGCATCCCAATTTGCAAGTGGGTCCCATCCAGGTTC 181

Db 241 CCCCTAAGCTCTGATCTGTAGTGCATCCCAATTTGCAAGTGGGTCCCATCCAGGTTC 300

Qy 182 GTGCAGTGTATCTGGACAGAGTTCATCTCCATCAGCAATCTGCAACCTGAAGACT 241

Db 301 GTGCAGTGTATCTGGACAGAGTTCATCTCCATCAGCAATCTGCAACCTGAAGACT 360

Qy 242 TTGCAAGTTACTACTGTCACAGAGTTACACTATATACCTTCGGCCCTGGGACCA 301

Db 361 TTGCAAGTTACTACTGTCACAGAGTTACACTATATACCTTCGGCCCTGGGACCA 420

Qy 302 AACTGGAGATCAACGA 318

Db 421 AGCTGGAGATCAACGA 437

RESULT 5

BG685444

LOCUS

DEFINITION 602637305F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4765129 5',

mRNA sequence.

ACCESSION BG685444

VERSION BG685444.1 GI:13916841

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 770)

NIH-MGC <http://mgs.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapps-f@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLC1623 row: i column: 02

High quality sequence stop: 713.

FEATURES

source

Location/Qualifiers

1. 770

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4765129"
/tissue="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 48"
/note="Organ: B-cells; Vector: pOTB7; Site:1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 84.6%; Score 269; DB 12; Length 770;
Best Local Similarity 90.5%; Pred. No. 1.3e-70;
Matches 287; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 2 AGCTCACCAGTCTCCATCTCCCTGCTGTGCTGTAGGACAGAGTCCACATCACTT 61
DB 80 AGATGACCCAGTCTCCAACTCCCTGCTGTGCTGTAGGACAGAGTCCACATCACTT 139
QY 62 GCCGGGACGTCAGAGTATAGCACCTATTTAAATGGTATCAGCAGAAACCGGGAAGG 121
DB 140 GCCGACAGAGTCAGAGATTTAGCAGCTATTTCAATGGTATCAGCAGAAACCGGGAAG 199
QY 122 CCCCTAAGCTCTGATCTGTAGTGATCCAAATTTGCAAGTGGGTGCCCATCCAGGTTCA 181
DB 200 CCCCTAAGCTCTGATCTGTGATCCAAATTTGCAAGTGGGTGCCCATCCAGGTTCA 259
QY 182 GTGGCAGTGGATCTGGGACAGAGTTCACCTTCACATCAGATCTGCAACCTGAAGACT 241
DB 260 GTGGCAGTGGATCTGGGACAGAGTTCACCTTCACATCAGAGTCTGCAACCTGAAGACT 319
QY 242 TTGCAAGTACTACTGTCAACAGAGTTACACTTATACCTTTCGSCCTGGGACCA 301
DB 320 TTGCAAGTACTACTGTCAACAGAGTTACACTTATACCTTTCGSCCTGGGACCA 379
QY 302 AACTGGAGATCAAAACGA 318
DB 380 AAGTGGATATCAAAACGA 396

RESULT 6

CB987347
LOCUS
DEFINITION
AGENCY: 13591809 NIH_MGC_184 Homo sapiens cDNA clone
IMAGE: 30326300 5', mRNA sequence.

CB987347
VERSION
KEYWORDS
SOURCE
ORGANISM

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 797)
NIH-MGC <http://imgc.ncbi.nih.gov/>.

Unpublished (1999)
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgaps@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LiNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: NDCM133 row: h column: 21

High quality sequence stop: 437.
Location/Qualifiers
1. 797

source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30326300"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site:1:
SfiI (ggccctatggcc); Site 2: SfiI (ggccctggcc); cDNA
Library is oligo-dT primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyroid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGGAGCGCGGCACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 84.6%; Score 269; DB 14; Length 797;
Best Local Similarity 90.5%; Pred. No. 1.3e-70;
Matches 287; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 2 AGCTCACCAGTCTCCATCTCCCTGCTGTGCTGTAGGACAGAGTCCACATCACTT 61
DB 106 AGATGACCCAGTCTCCATCTCCCTGCTGTGCTGTAGGACAGAGTCCACATCACTT 165
QY 62 GCCGGGACGTCAGAGTATTAGCACCTATTTAAATGGTATCAGCAGAAACCGGGAAGG 121
DB 166 GCCGGGACGTCAGAGTATTAGCACCTATTTAAATGGTATCAGCAGAAACCGGGAAGG 225
QY 122 CCCCTAAGCTCTGATCTGTAGTGATCCAAATTTGCAAGTGGGTGCCCATCCAGGTTCA 181
DB 226 CCCCTAAGCTCTGATCTGTAGTGATCCAAATTTGCAAGTGGGTGCCCATCCAGGTTCA 285
QY 182 GTGGCAGTGGATCTGGGACAGAGTTCACCTTCACATCAGCAATCTGCAACCTGAAGACT 241
DB 286 GTGGCAGTGGATCTGGGACAGAGTTCACCTTCACATCAGCAATCTGCAACCTGAAGACT 345
QY 242 TTGCAAGTACTACTGTCAACAGAGTTACACTTATACCTTTCGSCCTGGGACCA 301
DB 346 TTGCAAGTACTACTGTCAACAGAGTTACACTTATACCTTTCGSCCTGGGACCA 405
QY 302 AACTGGAGATCAAAACGA 318
DB 406 AAGTGGATATCAAAACGA 422

RESULT 7

CD705928
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CD705928
EST22455 human nasopharynx Homo sapiens cDNA, mRNA sequence.
CD705928
CD705928.1 GI:32236558
EST.
Homo sapiens (human)

Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 525)
Liu, X.-Q.; Zhou, Y.; Zhang, L.-J.; Xu, H.; Chen, H.-K.; Pan, Z.-G. and
Zeng, Y.-X.

Transcriptional Gene Expression Profile of Human Nasopharynx
Unpublished (2003)
Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China

Tel: 86-1380-9770-743

Fax: 86-20-8775-4506

Email: yxzen@gzsums.edu.cn.

Location/Qualifiers

source

```

FEATURES
    source
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            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /tissue_type="normal nasopharynx"
            /clone_lib="human nasopharynx"
            /note="ESTs generated from a normal nasopharynx cDNA
            library from southern Chinese"

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ORIGIN

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Query Match      84.1%; Score 267.4; DB 14; Length 525;
Best Local Similarity 90.2%; Pred. No. 3.1e-70;
Matches 286; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 2 AGCTCACCAGTCTCCATCCCTCCCTGCTGCTGTAGGACAGAGTCACCATCACTT 61
Db 124 AGATGACCCAGTCTCCATCCCTCCCTGCTGCACTGTAGGACAGAGTCACCATCACTT 183
QY 62 GCCGGGACGTCAGAGTATTAGCCTATTAAATTGGTATCAGCAGAAACCGGGGAAG 121
Db 184 GCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 243
QY 122 CCCCTAAGCTCTGATCTGTAGTCATCCAAATTTGCAAGTGGGTCCCATCCAGTTCA 181
Db 244 CCCCTAAGCTCTGATCTGTAGTCATCCAGTTTTCAAAGTGGGTCCCATCCAGTTCA 303
QY 182 GTGGCAGTGGATCTGGGACAGAGTTCACTTCACCATCAGCAATCTGCAACTGAAGACT 241
Db 304 GTGGCAGTGGATCTGGGACAGAGTTCACTTCGCAATCAGCAGTCTGCAACTGAAGATT 363
QY 242 TTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTGGCCCTGGGACCA 301
Db 364 TTGCAACTTACCTGTCAACAGAGTTACAGTACCGCTACACTTTTGGCCAGGGACCA 423
QY 302 AACTGGAGATCAACGA 318
Db 424 ACCTGGAGATCAACGA 440

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RESULT 8
CB985395
LOCUS
DEFINITION
    AGENCOURT_13643437 NIH_MGC_184 Homo sapiens cDNA clone
    IMAGE:30328513 5', mRNA sequence.
ACCESSION
    CB985395
VERSION
    EST.
KEYWORDS
    EST.
SOURCE
    Homo sapiens (human)
ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
    1 (bases 1 to 750)
    NIH-MGC http://mgs.nci.nih.gov/.
    National Institutes of Health, Mammalian Gene Collection (MGC)
    Unpublished (1999)
    Contact: Robert Strausberg, Ph.D.
    Email: cgabs-remail.nih.gov
    Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
    cDNA Library Preparation: CLONTECH Laboratories, Inc.
    CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LML)
    DNA Sequencing by: Agencourt Bioscience Corporation
    Clone distribution: MGC clone distribution information can be
    found through the I.M.A.G.E. Consortium/LML at:
    http://image.llnl.gov
    Plate: NDCM139 row: e column: 02
    High quality sequence stop: 555.

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FEATURES
    source
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            /organism="Homo sapiens"

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30328513"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
SfiI (ggccattatggcc); Site_2: SfiI (ggccctctggcc);
Library is oligo-dT primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyroid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCCATTTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGGAGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

```

ORIGIN

```

Query Match      84.1%; Score 267.4; DB 14; Length 750;
Best Local Similarity 90.2%; Pred. No. 3.8e-70;
Matches 286; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 2 AGCTCACCAGTCTCCATCCCTCCCTGCTGCTGTAGGACAGAGTCACCATCACTT 61
Db 104 AGATGACCCAGTCTCCATCCCTCCCTGCTGCACTGTAGGACAGAGTCACCATCACTT 163
QY 62 GCCGGGACGTCAGAGTATTAGCCTATTAAATTGGTATCAGCAGAAACCGGGGAAG 121
Db 164 GCCGGGACGTCAGAGTATTAGCCTATTAAATTGGTATCAGCAGAAACCGGGGAAG 223
QY 122 CCCCTAAGCTCTGATCTGTAGTCATCCAAATTTGCAAGTGGGTCCCATCCAGTTCA 181
Db 224 CCCCTAAGCTCTGATCTGTAGTCATCCAGTTTTCAAAGTGGGTCCCATCCAGTTCA 283
QY 182 GTGGCAGTGGATCTGGGACAGAGTTCACTTCACCATCAGCAATCTGCAACTGAAGACT 241
Db 284 GTGGCAGTGGATCTGGGACAGAGTTCACTTCACCATCAGCAGTCTGCAACTGAAGATT 343
QY 242 TTGCAAGTTACTACTGTCAACAGAGTTACACTTATATACCTTGGCCCTGGGACCA 301
Db 344 TTGCAACTTACTACTGTCAACAGAGTTACCGCTCCCTCGAAGCTTTCGGGAGGGACCA 403
QY 302 AACTGGAGATCAACGA 318
Db 404 AGTGGAGATCAACGA 420

```

```

RESULT 9
AW406886
LOCUS
DEFINITION
    UI-HF-BL0-adj-b-06-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
    IMAGE:3061499 5', mRNA sequence.
ACCESSION
    AW406886
VERSION
    AW406886.1 GI:6925943
KEYWORDS
    EST.
SOURCE
    Homo sapiens (human)
ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
    1 (bases 1 to 431)
    NIH-MGC http://mgs.nci.nih.gov/.
    National Institutes of Health, Mammalian Gene Collection (MGC)
    Unpublished (1999)
    Contact: Robert Strausberg, Ph.D.
    Email: cgabs-remail.nih.gov
    Eco RI site shown at the beginning of the sequence.
    Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
    CDNA Library Preparation: M.B. Soares Lab
    CDNA Library Arrayed by: M.B. Soares Lab
    DNA Sequencing by: M.B. Soares Lab
    Clone distribution: MGC clone distribution information can be

```

